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AX086257 Bacillus
I32627 Bacillus
I3202 Bacillus th
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Listing first 45 summaries
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ALIGNMENTS

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Bacillus thuringiensis Bacillus thuringiensis Bacteria; Firmicutes; Bacillales;		Bacillaceae, Bacillus,	llus;	Bacillus	llus
Arnaut, G., Boets, A., Damme, N., Mathieu, E., Vanneste, S.	chieu, B.,	Vanneste		and van	
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RTYPINTSAQLTREVYTDALGATGYNMASMMYNNNAPSFSALETAVIRSPHILDFLE QLTI FSTSSRMSATRHMTYMRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLSFFSRDV YMTESYAGVILMGTILEPIGVPTVRRPRNPNPONTFERGTANYSOPYESPGLOLKODS	VNMASMNWY IQSRPIGGG VRFNFRNPC	INNNAPSFSA LINTSTHGST NTFERGTAN	IETAV NTSIN YSOPY	TRSPHI PVRLS ESPGL(LLDFLE PFSRDV DLKDSE
TELPPETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRTNTISSDSITQIP LVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ	LI SQSRVHV I RTNVNGSV	PVYSWTHRS TSMGLNFNN	ADRTN TSLOR	TISSDE	SITOIP
TMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQTAGISISNNA GRQTFHFDXIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHDQVSN	NESLTSQSF LERAQEAVN	'r fabfpvgi Ial ftntnpr	SASGS	OTAGIE	ISNNA
LVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEGSNFT SIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQXIGESELKAYTR	KRLSDERNI FKENYVTLF	LODPNFTSI GTFNECYPT	NKOPD YLYQK	FISTN	KAYTR

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Query Match Best Local S: Matches 3687

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YQLRGYIEDSQDLEIYLIRYNAKHETLDVPQTESVWPLSVESPIGRCGEPNRCAPHFE WNPDLOCSCTROGRCAHHSHHPSLDIDIGCTDLHENLGWWVFKLKTQEGHARLGNLE WNPDLOCSCTROGRCAHHSHHPSLDIDIGCTDLHENLGWWVFKLKTQEGHARLGNLE PREBEDLIGGALSKYRXAEKKWRDKGRKLQLETKRVYTERKEAVDALFVDSQYRRLQN DTNIGMIHAADKLVHRIREAYLSELSVIJEWNBETFRELEGRIITAISIYDARNVYKN DTNIGMIHAADKLVHRIREAYLSELSVIJEWNBETFRELEGRIITAISIYDARNVYKN DTNIGHTWRCHVTYGORGYTLRVYKEG GDPNNGTACWNKGHVDYGGHRAYEGBA YGGCYTLIRITAINYEGHTYEBLKFKNGEBERVY PTDTGTCNDYTAHQGTRAVCRSRAATEDA YRUDTTASVNAKETYEETTYTDVRRDHCEYDRGYWYPPLPAGYMTKELEYFPETDK VHIEIGETEGKFIVDSVELLLMEE" ö Gaps .. Length 3687; Indele ô atch 100.0%; Score 3687; cal Similarity 100.0%; Pred. No. 0; 3687; Conservative 0; Mismatches

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3061 CTATACGATGCGAGAAATCTCGTTAAAAATGGTGATTTTAATAATGGATTAGCATGCTGG 3121 AATGTAAAAAGGGCATGTAGAAGAGCCATCACCGTTCTGTCTG	DD 3121 AATGTAAAAGGGCATGTACAACAGAGCCATCACCGTTCTTGTTATCCCA 3180 QY 3181 GAATGGGAAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTATATCCTC 3240	OY 3301 AACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAAGAGTGTATCCAACGGAT 3360	Qy 3361 ACAGGAACGTGATATACTGCACCACCAGGTACAGCAGTATGTAATTCCCGTAAT 3420	Qy 3421 GCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATTTAATTACAAACCGACT 3480 Db 3421 GCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATAAAACCGACT 3480	Qy 3481 TATGAAGAAACGTATACAGATGTACGAAGAGATAATCATTGTGAATATGACAGAGGG 3540	Qy 3541 TATGTGAATTATCCACCACTACCAGGTTATATGACAAAGAATTAGAATACTCCCA 3600 Db 3541 TATGTGAATTATCCACCACTACCAGGTGGTTATATGACAAAGAATTAGAATACTTCCCA 3600	Qy 3601 GARACCGATARGGATTGAGATTGGAGAAGGGAAGGTTTATTGTAGACAGC 3660	Qy 3661 GTGGAATTACTCCTTATGGAGAATAG 3687 Db 3661 GTGGAATTACTCCTTATGGAGAATAG 3687	AR359382	TION Sequence 37 from patent. ION AR359382 GI:33765692 DS	Unknown. Unknown. Unclassified. 1 (bases 1 to 4173)	S Baum, J.A. Lepidopte Compositi	FEATURES LOCALION QUALILIEES 1 . 4173 /organism="unknown" /mol_type="genomic DNA"	tch 99.4%; Score 3666.2; DB 6; Length 4173; al.Similarity 99.6%; Pred. No. 0;	MATCHES 30/4; CONSEIVE 0; MISMATCHES 13; INCELS 0; CAPS 0; QY 1 TICACTICAAATAGGAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA 60
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	2461	AAACATGAAACATTGGATGTTCCAGGTACCGTATGGCCGCTTTCAGTTGAAAGC 2520	ර සි	354
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	2581	CTAGATTGTTCCTGCAGAGATGAGAAAAATGTGCGCATCATTCCCATCATTTCTCTTTG 2640	qq	366
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baum, J.A., Chu, C.R., Donovan, W.P., Gilmer, A.J. and Rupar, M.J. Lepidopteran-active bacillus thuringiensis delta-endotoxin compositions and methods of use Patent: WO 011989-3 37 22-MAR-2001; MONSANTO COMPANY (US)
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YGBGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAACNSRNAGYEDA YEVDTTAAVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLBAGYVTKELBYFPETDK VWIEIGETEGTFFUDSIFLLLAMEE"			OY 1	Db 1 TTGACTTCAAATAGGAAAATGAAATGAAATGAAATGAGGATTGTTTGTGT 120	OY 61 TGGAATGATTCCACACAAATGGATGTTTTTTTTTTTTTT	121 ATAGCCGAGGGAATAATATCAATCCACTTGTTAGCGCATCAACAGTCCAATT		OY 181 AACATAGCTGGTAGATACTAGGTGTATTAGGCGTACCGTT[181 AACATAGCTGGTAGAATACTGCTGCTGCTGCTGCTGTGGTGGGAATTTTC	241	241 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 301 CIAGAATACGGCA 360 THINITITITITITITITITITITITITITITITITITIT	361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTGACAGTTAGAAGATTAGAAGATTAGAAGAATTAGAAGAATTAGAAGA	Db 361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATATATA	Qy 421 TGGCTAGAAAACCGTGATGATGATAACAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	421 TGGCTAGAAAACCG.GA.GA.GA.GA.GA.GA.GA.GA.GA.TTTCGCAATTAGAAACCAAGAAGTTCCA	*81	481 TIAGARCTICATOR AND TOTAL AND TOT	541 TTATTANICATION TO THE STATE OF THE STATE	601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA		661 GTGGAACAAAGGAGATTATTCCGACTATTGCGTAGAATGGTAATAALAAAT	Db 661 GTGGAACGAGAGATTATTCCGACIALISCOLAGOTTATAGAGAGATCTA 780	Oy 721 AGCTTGAGAGACAAATGCCGCAAA115CGCTTGAGTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTT		781 ACGTTAGGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	/81 ACGIIIICOGGAACTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCACACAGGGAAGTTTATACAAGGGAAGTTTATACAAGGGAAGTTTATACAAGGGAAGTTTATACAAGGGAAGTTTATACAAGGGAAGTTTATACAAGGGAAGTTTATACAAGGGAAGTTTATACAAGGGAAGTTTATACAAGGGAAGTTTATACAAGGGAAGTTTATACAAGAGAAGTTTATACAAGAGAAGTTTATACAAGAAGTTTATACAAGAGAAGTTTATACAAGAGAAGTTTATACAAGAGAAGTTTATACAAGAGAAGTTTATACAAGAGAAGTTTATACAAGAGAAGATTATACAAGAGAAGATTATACAAGAGAAGATTATACAAGAGAAGATTATATACAAGAGAAGATTATATACAAGAGAAGATTATATATA	dy 841	901 GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCTAAAAAA	

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CCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAATCCTGAT
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Bacillus thuringiensis CrylBel delta-endotoxin gene, complete cds.
AATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCCTTGTTATCCCA 3180
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Bacillus thuringiensis
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Payne, J., Cuminge, D.A., Cannon, R.J.C., Narva, K.E. and Stelman, S.J. Bacillus thuringiensis genes encoding lepidopteran-active toxins
Patent: US 5723758 03-MAR-1998,
Mycogen Corporation; San Diego, CA
                                                                                                                                                                            3301 AACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCAACGGAT
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Submitted (08-JUL-1998) Molecular Biology, Mycogen Corporation,
5501 Oberlin Dr., San Diego, CA 92121, USA
Location/Qualifiers
                                             GAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTCTCCCGGGGCGTGGCTATATCCTC
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AUTHORS Payne, J., Cummings, D.A., Cannon, R.J.C., Narva, K.E. TITLE Bacillus thuringiensis genes encoding lepidopteran- JOURNAL Patent: US 5723758-A 7 03-MAR-1998; FRATURES Location/Qualifiers	2815 AAACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTG 2874 	& g
SOURCE Unknown. ORGANISM Unknown. The state of the state	2755 AAACCATTATTAGGAGAAGCACTGTCTGGTGAAGAGAGAG	දු දු
Sequence / Irom parent US 3/23/3 190319 190319.1 GI:3410259	2695 TTCAAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAG 2754 	ර් සි
RESULT 5 190319 LOCUS LOCUS DRFNITTION Sequence 7 from patent US 5723758.	2635 TCTTTGGATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTGTGGTGTG 2694 2632 TCTTTGGATATTGATGTTGGATGCATAGACTTGCATGAGAACCTAGGCGTGTGGGTGTGGGTA 2691	පි සි
3652 GACAGCGTGGAATTACTCCTTATGGAGGAATAG	2575 CCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAATGTGCGCATCATTCCCATCATTTC 2634 	& g
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3415	2335 IGTTAICCGACGTATTTAIATCAAAAATAGGAGAGTCGGAATTAAAAGCTTATACTCGC 2394 	දි දි
3355	2275 CAGGAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAG 2334 	୫ ୍ଶ
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<pre>gource 13684 /organism="unknown" /mol_type="unassigned DNA"</pre>	Query Match Best Local Similarity 93.4%; Score 3266.6; DB 6; Length 3684; Best Local Similarity 93.4%; Pred. No. 0; Matches 3449; Conservative 0; Mismatches 229; Indels 15; Gaps	TTTATCGATTCCAG				241 TITTATAGITTICITGGIGAATTATGGCCCGGGGGGAGATCAGIGGGAAATTITC 300 	CGCCA 	AAGAT	ragec 	481 TTAGAACTIGATITICTIAATGCGTGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540 	_		661 GTGGAACAAACGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720 	721 AGCTTGAGGGACAAATGCGCGAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 780 	781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840 	841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG 900 	10001 	

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Direct Submission
Submitted (26-JAN-1988) Whiteley H. R., Department of W. Department
of Microbiology, University of Washington, Seattle, WA 98195
Location/Qualifiers
                                                                                                                           BCT 10-FEB-1999
                                                                                                                                                                                     cryA4 gene; crystal protein; delta-endotoxin; endotoxin.
Bacillus thuringiensis
Bacillus thuringiensis Bacillacese; Bacillus than Bacillus Bacteria; Firmicutes; Bacillus
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Brizzard,B.L. and Whiteley,H.R.
Nucleotide sequence of an additional crystal protein gene cloned
from Bacillus thuringiensis subsp. thuringiensis
Nucleic Acids Res. 16 (6), 2723-2724 (1988)
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    note="unnamed protein product; delta-endotoxin (AA)

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/mol_type="genomic DNA"
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1731 GTTGTTAGAGGACCAGGATTTACTGGTGGGGATATTCTTCGAAGAACGAATACTGGTGGA 1621 GTACTAAGTATGGGTTATTTAATAATAATACATCATTACAGGGTATCGGTGAGAGT 1791 TTGGACCGATAAGATAACTGTTAACGGACCATTAACACAAAGATTCGTATAGGATTTT 1681 CGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGAGTACTTTTTTTT		ACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGGGGGGAATGCT 	GTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAGAGAAAGAGAAAGAGAAAGAGAAAGAGAAAGAGAAAGAG	AACTTCACATCCATCAATAAGCAACCAGGATTCATATCTACTAATGAGCAATCGAATTCA AACTTCACATCCATCATAAGCAACCAGACTTCATATCTACTAATGAGCAATCGAATTTC AACTTCACATCCATCAATAAGCAACCAGACTTCATATCTACTACTAGAGCAACCGAATTTC ACTTCACCATCCATCAATAAGCAACCAGACTTCATATCTACTAGAGCAACATTACAATCCAG ACATCTATCCATCAATAATCTCAAAATGATGATGATGGAGAAACATTACAATCCAG	GAAGGAAATGACGTATTTAAAGAGAATTACGTCACACATACGGGGACTTTTAATGAGTGT [CAATTAAGAGGTATATTGAAGATAGTCAAGATTAGAGATATATTGATTCGTTATAAT [AGCCCAATGGAAGTIGGAGAACGGAACGGACGGCGCCCAATGGACGGTTGAAAAAATGTGAATGGAAGGAA	TIGGATATIGATATIGGATGCACAGACTIGCATGAGAATCTAGGCGTGTGGGGTGGTATIC

Oy 781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840	1021 ACTTCATCACGATGAGCTACTAGGCATATGACTTACTGGCGGGGGCACACAATTCAA	1141 1311 1201 1371	1261 TTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCCTATGG 1	1381 CCAAATTATGAATCATAATCATAGGTTATCTCACATAGGGCTCATTTCACAATCTAGG	1501 TCAGATAGCATAACCATTGGTAAATTCATTCAGGTACCTCT	1621 GTACTAAGTATGGGTCTTAATTATAATACATCATTACAGCGGTATCGCGTGAGAGTT	1741 GATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCATTTAGA
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ACCESSION ACCESS	Query Match 85.0%; Score 3133.6; DB 6; Length 4074; Best Local Similarity 91.1%; Pred. No. 0; No. 0; Matches 3373; Conservative 0; Mismatches 299; Indels 30; Gaps 3; Qy 1 TTGACTTCAAATAGGAAAAATGAAATTATAAATTATAAATGCTTTATCGATTCCAGCTGTA 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TGTGT 					

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                    CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCT
                                            CTTGCTCGATTACAAGGTTTAGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT
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                                                /sub species="entomocidus"
/db_xref="taxon:1436"
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/note="BtII promoter"
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	-	NEGRALSM Unknown. REPERENCE 1 (bases 1 to 3934) AUTHORS DONOVAN,W.P. Tan,Y. Jany,C.S. and Gonz alez,Je.M. Jr. TITLE Bacillus thuringiensis cryETS gene and related plasmids, bacteria and insecticides JOURNAL Patent: US 5516319-A 3 01-APR-1997; BOURCE 1. 3934	268 40.	1 TIGACTICCAATAGGAAAATGAGAAIGAAATTATAAATGCTTIATCGATICCAGCIGTA 60 	61 TCGAATCATTCCACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGTT	121	307	301	361	421	481 547	OY 541 TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTGAGAGATGCCTCT 600 	

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GTAAGGATTCGTTATGCTTCTACTACAGATTTACAATTTTTCACGAGAATTAAATGGAACC ACTACTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAA ACTACTTTAATATTGCAGAATTTCTCAAGAACTATGAATAGGGGGGATAATTTAGAATATAGA TCATTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGA TCATTTAGAATTTGCAGAATTTTCCTGTAGGTATTAGTGCATCTGGCAGCCAAACTGCTGGA AGTTTTAGAACTGCAGATTTAGTACTCCTTTTAAATTTTAAAATGCAAAGCACATTC ATAAGTATAAGTAAAAATGCAGGTAGAAACGATTCACTTTGATAAAATTGAATTCATT	1921 ACATTGGGTGCTCAGAGGTTTTTCAAATCAGGAAGTTTATATAGATAG	GATCAAGTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAAAGAGA	2212 AATTCACATCTATCCATGAACAATCTGAACATGCGGGGAAGTGAGGAACATACA 2280 2212 AATTTCACATCTATCCATGAACAATCTGAACATGGATGGGGAAGTGAGAACATTACA 2271 2281 AACTTCCCTCTATTAATGAGCTATCTGAACATGGATGGGGAAGTGCGAATGTTACC 2340 2272 ATCCAGGAAGGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAAT 2331 2341 ATTCAGGAAGGAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAAT 2300	2332 GAGTGTTATCCGACGTATTATATCAAAAATAGGAGAGTCGGAATTAAAAGCTTATACT 2391 [2521 TACAATGCAAAGATTGGATGTTCCAGGTACCTTTCCTTT	2632 THCTCTTTGGATATTGATGATGCACAGACTTGCATGAAATCTAGGGGTGTGGGTG 2691 2701 TTCACTTTGGATATTGATGTTGGTGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTG 2692 GTATTCAAGATTAAGACGCAGGAAGGTCATGCAAGATTGGGAATTTATTGAA 2751 2761 GTATTCAAGATTAAGACGCAGGAAGGTCATGCAAGATTAGGAATTTATTGAA 2751 2761 GTATTCAAGATTAAGACGCAGGAAGGTTATGCAAGATTAGGAATTTATTGAA 2820 2752 GAGAAACCATTATTAAGAAGAAGGTTTCGTGTGAAGAAGAAGAAGAAAAATTGAAGA 2811

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- nucleic search, using sw model OM nucleic

November 21, 2004, 08:48:00; Search time 1565 Seconds (without alignments) 12367.166 Million cell updates/sec Run on:

US-10-614-524-1 3687

1 ttgacttcaaataggaaaaa.......tactccttatggaggaatag 3687 Title: Perfect score: Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

4134886 segs, 2624710521 residues

Searched:

8269772 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_23Sep04:* Database :

geneseqn1980s:* geneseqn1990s:*

geneseqn2003cs:*geneseqn2003ds:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2003as:* geneseqn2003bs:* geneseqn2002bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:

		d			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length DB	B	QI	Description
н	3687	100.0	3687	4	AAH28240	Aah28240 Nucleotid
8	3666.2	99.4	4173	4	AAS02482	Aas02482 B. thurin
٣	3266.6	88.6	3684	~	AAV15222	Aav15222 Bacillus
4	3266.6	88.6	3684	4	AAA89221	Aaa89221 Bacillus
S	3260.2	88.4	3684	4	AAS02489	Aas02489 B. thurin
9	3132	84.9	4074	~	AAQ56804	Aaq56804 Bacillus
7	2687.2	72.9	3932	~	AAQ64112	Aaq64112 cryET5 ge
80	2687.2	72.9	3932	0	AAZ09160	
6	2687.2	72.9	3934	~	AAT95051	Aat95051 DNA encod
10	2687.2	72.9	3934	~	AAT68434	Aat68434 CryET5 ge
11	2687.2	72.9	3934	~	AAV83927	Aav83927 DNA encod
12	2684.2	72.8	3687	12	ADK98478	Adk98478 B thuring
13	2630.2	71.3	3627	4	AAS04854	Aas04854 Bacillus
14	2544.4	0.69	3663	4	AAS00422	Aas00422 B. thurin
15	2541.2	68.9	3663	4	AAS00421	Aas00421 B. thurin
16	2384.2	64.7	3624	4	AAS04853	Aas04853 Bacillus
17	2004.8	54.4	3651	4	AAS04852	Aas04852 Bacillus
18	1793.4	48.6	3522	~	AAT16558	Aat16558 B.t. toxi
19	1791.8	48.6	3522	7	AAQ06830	Aaq06830 Sequence
20	1791.8	48.6	3522	0	AAT49592	Aat49592 Bacillus
21	1790.2	48.6	3522	7	AAQ26928	Aaq26928 DNA encod

22	1662	45.1	4106	7	AAV16214		Aav16214 DNA encod
23	1662	45.1	4106	7	AAV09318	a	Aav09318 Bacillus
24	1581.6	42.9	3558	~	AAX60619		Aax60619 Polynucle
52	1501	40.7	3766	7	AAQ77858		Aaq77858 Crystal p
56	1438.6	39.0	8854	~	AAZ20086		Aaz20086 DNA encod
27	1432.4	38.9	3713	7	AAQ64111		Aag64111 cryET4 ge
28	1432.4	38.9	3713	7	AAT95050		Aat95050 DNA encod
29	1432.4	38.9	3713	7	AAT68435		Aat68435 CryET4 ge
30	1432.4	38.9	3713	~	AAV83926		Aav83926 DNA encod
31	1432.4	38.9	3713	7	AAZ09159		Aaz09159 B. thurin
32	1411.4	38.3	4020	~	AAQ14648		Aaq14648 crylF gen
33	1408.4	38.2	3522	N	AAQ10182		Aaq10182 Lepidopte
34	1408.4	38.2	3522	7	AAQ47291		Aaq47291 Delta end
35	1408.4	38.2	3522	7	AAV62081		Aav62081 Plasmid p
36	1408.4	38.2	3522	~	AAX60606		Aax60606 Wild-type
37	1408.4	38.2	3522	4	AAS00565		Aas00565 B. thurin
38	1406.8	38.2	3522	~	AAT18722		Aat18722 Codon-rew
39	1405.2	38.1	3522	~	AAT05270		Aat05270 CryIF tox
40	1402.2	38.0	5170	12	ADK98488		Adk98488 B thuring
41	1402.2	38.0	2600	12	ADK98490		ф
42	1402.2	38.0	9	12	ADK98482		Adk98482 B thuring
43	1402.2	38.0	7000	12	ADK98485		Adk98485 B thuring
44	1402	38.0	3534	~	AAV31162		Aav31162 Bacillus
45	1402	38.0	3534	9	ABK11833		Abk11833 DNA encod

ALIGNMENTS

CrylBf, insecticidal protein; CrylJd; Cry9Fa; lepidoptera; coleoptera; insect pest; transgenic plant; ss. Nucleotide sequence of a CrylBf insecticidal protein. AAH28240 standard; DNA; 3687 BP. 05-SEP-2001 (first entry) Bacillus thuringiensis. AAH28240; RESULT 1 AAH28240

Location/Qualifiers
1. .3687
/*tag= a /product= "CrylBf insecticidal protein" Key

WO200147952-A2

05-JUL-2001.

19-DEC-2000; 2000WO-EP013184.

99US-0173387P. 28-DEC-1999; (AVET) AVENTIS CROPSCIENCE NV.

Van Rie J; Vanneste S, Damme N, Mathieu E, Arnaut G, Boets A,

WPI; 2001-425619/45. P-PSDB; AAB84628.

Novel insecticidal proteins CrylJd, Cry9Fa and Cry1Bf, derived from Bacillus thuringiensis, useful for controlling insects in plants.

Claim 5; Page 30-36; 65pp; English.

The present sequence encodes CrylBf, an insecticidal protein derived from Bacillus thuringiensis. The specification also describes Cryld and Cry9Fa. The Cry proteins have actificatist lepidopteran and cloopteran insect pests. Cry1Bf, Cry1Ad and Cry9Fa polynucleotides and

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1381 CCAAATTATGAATCATAGTCATAGGTTATCTCACATAGGGCTCATTTCACAATCTAGG
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polypeptides are useful for obtaining a plant with resistance to insects. Cry polynucleotides are useful for producing transgenic plants which are resistant to insects
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100.0%; Score 3687;
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CGTGTCACAGCGTACAAAAGAGGGATATGGAGAGGGGTTGTGTAACGATCCATGAATCGAG
                                                                                                                                                                          GCTGGATATGAGGATGCATATGAAGCTGATACTACAGCATCTGTTAATAACAAACCGACT
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    B. thuringiensis DNA encoding a toxic crystal protein, CryET64.

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1. .3471
/*tag= a //rtag= //rtag= //rtansl_except= (pos:1...)
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The sequence encodes a B. thuringlensis Lepidopteran-active delta-
c andotoxin, crystal protein CryEr64. The Lepidopteran-active B.
thuringlensis delta-endotoxin polypeptides may be used as compositions
that are applied to plant crops to protect them from insect damage. The
polymuclectides may be used in the production of transgenic plants that
express the insecticidal polypeptides and consequently have improved
insect resistance compared to non-transformed plants. Monocotyledonous or
cotyledonous plants may be protected in this way, for example corn,
wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, fomato,
tobacco, kapok, flax, potato, baley, turf grass, pasture grass, berry,
cobacco, kapok, flax, potato, baley, turf grass, pasture grass, berry,
fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
cotton leaf perforator and spruce budworm) may be affected by application
cotton leaf perforator and spruce budworm) may be affected by application
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                                                                                                                     Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the insect resistance of plant.
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99.4%; Score 3666.2; DB 4; Length 4173;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3674; Conservative 0; Mismatches 13; Indels 0;
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                                     Rupar
                                   Gilmer AJ,
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                                   Donovan WP,
                                                                   WPI; 2001-281518/29.
P-PSDB; AAU02039.
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1021 ACTICATCACGATGGAGTGCTACTAGGCATATGACTTACTGGCGGGGGGCACACAATICAA 1080 TITAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCCTATGAG 1320 CTTTTTGCTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA GTGGAACAAACGAGATTATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT AGCTTGAGAGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTA 721 AGCTTGAGAGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGATCTA ACGITAGGGGTATITAGATCTAGTGGCACTATTCCCCAAGCTATGACACTCGCACTTATCCA 841 ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGGAACAAGGG 901 GTABATATGGCAAGTATGAATTGGTATAATAATAATGACCCTTCGTTTTCCGCTATAGAG 961 ACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATTTTTAGC CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAA ATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGACGCAATTGGAGCAACAGGG GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCTATAGAG 961 ACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATTTTTAGC 1081 TCTCGGCCAATAGGAGGGGGATTAAATACCTCAACGCATGGGTCTACCAATACTTCTATT TCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCAATACTTCTATT TTTAGGAACCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCCTATGAG TCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACAACGA TCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACAACAGAACGA CCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTCACAATCTAGG AATCCTGTAAGATTATCATTCTTCTCGAGACGTATATTGGACTGAATCATATGCAGGA GTGCTTCTATGGGGAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTTAGATTTAAT 1381 CCAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTCACAATCTAGG GTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACCATTAGT GTAGTCAGTGGCCCAGGATTTACAGGAGGGGATATAATCCGAACTAACGTTAATGGTAGT GTACTAAGTATGGGTCTTAATTAATAATACATCATTACAGGGGTATCGCGTGAGAGTT GTACTAAGTATGGGTCTTAATTTTAATAATAATACATCATTACAGCGGTATCGCGTGAGAGTT GTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACCATTAGT TCAGATAGCATAACACAAATACCATTGGTAAAATCATTCAACCTTAATTCAGGTACCTCT 601 601 661 721 781 1081 1321 841 901 1141 1141 1201 1261 1261 1321 1381 1441 1621 1201 1441 1501 1501 1561 1561 1621 셤 Š 유 8 셤 셤 셤 ਨੇ à ઠ 셤 ð 엄 셤 유 ò ઠે Š д Š g Š 셤 ઠ g ઠ 원 ઠે 셤 ò g ઠે 셤 셤 ò 120 180 240 900 9 180 240 300 420 480 480 540 540 9 9 Gapa

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Db 2761 TTATTAGGAGAGCACTGTCTCGTGTGAAGAGCAGAGAAAAATGGAGAGAGA	Oy 2821 GAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTGGATGCT 2880 Db 2821 GAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTGGATGCT 2880	2881	2941	3001	Qy 3061 CTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTAGCATGCTGG 3120 Db 3061 CTATACGATGAGAAATGTCGTTAAAAATGGTGATTTTAATAATGATTAGCATGCTGG 3120	3121 AATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTTGTTATCCCA 3121 AATGTAAAAGGGCATGTAGAATGTACAAGAGGCCATCACCGTTCTGTCTTGTTATCCCA	3181 GAAIGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTATTCCTC	3241 CGTGTCACAGCGTACAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAAATCGAG 	3301 AACAATACAGAGCAACTAAAATTTAAAAACTGTGAAGAAGGAAG	3361 3361	3421 GCTGGATATGAGGATGCATATGAGTTGATGATGAGCATCTGTTAATTACAAACCGACT 	3481 3481	3541	3601	Oy 3661 GTGGAATTACTCCTTATGGAGAATAG 3687 Db 3661 ATAGAATTACTCCTTATGGAAGAATAG 3687	RESULT 3 AAV15222 ID AAV15222 standard; DNA; 3684 BP.	AX AAV15222; XX DT 27-MAY-1998 (first entry) XX DE Bacillus thuringiensis 158C2c toxin encoding DNA.
1681 CGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGAGTACTACTTTT 1740 	1741 GATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATTAGA 1800 	TTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCGGTCAAACTGCTGGAATAAGTATA	TTACT TTACT	1921 GCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAATGCTCTGTTT 1980 	1981 ACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAAGTA 2040 	2041 TCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAGAGAGAATTACTT 2100 	2101 GAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAA	2161 TTCACATCCATCAAGCAACCAGACTTCATATTACTAAGCAATCGAATTTCACA 2220 	2221 TCTATCCATGAACATCTGAACATGGTGGGGAAGTGAGAACATTACAATCCAGGAA 2280 	2281 GGAAATGACGTATTTAAAGAGAATTACGTCACCTACCGGGGACTTTTAATGAGTGTTAT 2340 	2341 CCGACGTATTTATATCAAAAATAGGAGACTGGAATTAAAAGCTTATACTCGCTACCAA 2400 	2401 TTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAATGCG 2460 		2521 CCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGGAATCCTGAT 2580 	2581 CTAGATTGTTCCTGCAGAGAGAGAAAATGTGCGCATCATTCCCATCATTTCTCTTTG 2640 	2641 GATATTGATATTGGAGACAGACTTGCATGAGAATCTAGGGGTGTGTGGGTGG	2701 ATTAAGACCCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAAACCA 2760

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1075 ATTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCAATACT 1134
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                         CTAGAACATGTCGAACAACTTATAAGACAACAAGTAACAGAAAATACTAGGGATACGGCT
                                                                                                     CTTGCTCGATTACAAGGTTTAGGAAATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT
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                                                                                                                                             TGGCTAGAAAACGGTGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a 158C2c toxin from Bacillus thuringiensis. The present invention describes isolated nucleic acid sequences encoding toxins active against lepidopteran insects. The present invention also describes a recombinant host transformed with a nucleic acid sequence encoding a toxin. The nucleic acid sequence can be amplified. The product lepidopteran pests. N.B. The numbers in the sequence listing do not correspond to the SEQ ID No: 4, 5 and 6 are said to correspond to the sequences encoding the toxins, and SEQ ID No:7, 8, 9 and 10 are said to correspond to the amino acid sequences of the toxins, whereas in the sequence listing the amino acid sequence is given after the nucleic acid sequence listing the amino acid sequence is given after the nucleic acid sequence encoding it (i.e. SEQ ID No:3 encodes SEQ ID No:9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                thuringiensis; 158C2c; toxin; lepidopteran-active; insect; transgenic plant; resistant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding Bacillus thuringiensis toxin proteins - for producing transgenic plants resistant to attack by lepidopteran pests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3684;
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Pred. No. 0;
0; Mismatches 229; Indels
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                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Cummings
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Best Local Similarity 93.4%;
Matches 3449; Conservative (
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93US-00069902
                                                                          thuringiensis.
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01-JUN-1993;
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                                      microbe;
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<i>&</i>	a &	a 5	≩ 8	상 옵	<i>&</i> ∄	<i>&</i> 8	<i>⋧</i> 8	<i>ò</i> ₽	<i>&</i> ₽	& A	<i>⋧</i> 8	8 3	දි සි	승 옵	는 A 	ጵ	상 용	δ a
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TCGAATCATTCCGCACAAATGAATCTATCAACCGATGCTCGTATTGAGGATAGCTTGTGT 120
                                                  AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT
                                                                                                              TTTTATAGTTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC
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                  This is the partial nucleotide sequence of the novel delta-endotoxin 1582Cc gene of Bacillus thuringiensis (B.t.) isolate PSISBC2 (NRRL B-18872). To isolate novel toxin genes from PSISBC2, total cellular DNA was subjected to PCR amplification using primers (see AAA89222-23) based on conserved sequences of B.t. toxins. The PCR products were used as probes to screen a PSISBC2 gene library. Plasmid subclone pMYC2383 was obtained which contained the entire coding sequence for 158C2c (see AAA8921), the 3 portion of the 158C2b gene (see AAA89220) and the 5' portion of 158C2b pMYC2387. These novel genes encode delta-endotoxins (see AAB9218). that are active against lepidopteran pests. Expression in transformed plants confers resistance to such pests, while transformed microorganisms expressing the delta-endotoxins can be applied to sites where they will
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                                                                                                                                                                                                                                                                                                     Delta-endotoxin; 158C2c; toxin; lepidoptera; crystal protein;
transgenic plant; insect resistance; crop protection; biological control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genes isolated from Bacillus thuringiensis which encode toxins against lepidopteran insects and which can be used to transform various hosts to express the B.t. toxin and confer insect resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGACTTCAAATAGGAAAAATGAGAAATGAAATTATAAAATGCTTTATCGATTCCAGCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cannon RJC;
                                                                                                                                                                                                                                                                      Bacillus thuringiensis delta-endotoxin gene 158C2c
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                                                                               GACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                         DNA; 3684
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93.4%;
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Best Local Similarity 93.4
Matches 3449; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis.
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QY 2275 CAGGAAGTGAATTAAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGGG 23 Db 2272 CAGGAAGTAATTAAAAGAGAATTACGTCATACTACCGGGACTTTTAATGAG 23 QY 2335 TGTTATCCGACGTATTTATCAAAAATAGGAGAGTCGGAATTAAAAGCTTATACTCGC 23 Db 2332 TGTTATCCGACGTATTTATATCAAAAATAGGAGAGGCGGAATTAAAAGCTTATACTCGC 23 QY 2395 TACCAATTAAGAGGGTATATTATAAAAATAGAGGTGAGAATTAAAAGCTTATACTCGC 23 Db 2392 TACCAATTAAAGAGGGTATATTGAAGATGCAAGATTTAGAGATATTTGATTCGTTAT 24 Db 2392 TACCAATTAAAGTGCATATATTGAAGATAGTCAAGATTTAGAGATATTTGATTCGTTAT 24 Db 2392 TACCAATTAAGTGCATATATTGAAGATAGTCAAGATTTAGAGATATTTGATTCGTTAT 24	2455 AATGCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCAGTT 2 [CCAATCGGAAGGTGCGGAAACCGAATCGATGCGCACCACATTTCCCCTGATCGATGGGGAAAAATGTGCGCATCATTCCCTGCAGGAAGGGGAAAAAATGTGCGCATCATTCCCTAGATTGCAGAAAAAATGTGCGCATCATTCCTTAGATTGTGCGCATCATTCCCTGCAGAAAAAATGTGCGATCATTCCTTGCTGAAAAATGTGAAAAATGTGCAATCATGCAATGAAAAAATGTGAAAAAAAA	2632 TCTTGGATATTGATGTTGGATGCATAGACTTGCATGAGAACCTGGGGTGGGT	2755 AAACCATTATTAGGAGAAGCACTGTCTCGTGAAGAGAGCAGAGAAAAATGGAGGAGAC 2	DD 2812 MARCELGRANGELOCIES 2811 QY 2875 GAIGCTTTATTGTAGATTCTCAATATAATAGATTACAAGGGATACAAAACATGGCATG 2934 DD 2872 GAIGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGGGATACAAACATTGGCATG 2934	2935 ATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGCTTATCTGTCAGAATTATCT 2	OY 2995 GTTATCCCGGGGTGTAATGCGGAATTTTTGAAGAATTTAGAAGATGCGCATTATCACTGG 305- Db 2992 GTTATCCCAGGTAAATGCGAAATTTTTGAAGAATTTTAGAAATTTAGAAAATGCGATTATCACTGG 305- OY 3055 ATCTCCCTATACGACAAATGCGTTAAAAAATGCTGATATTAATAATAAAAAGATTAGAATTTAATAATAAAAATGGATTAGGA 311-	Db 3052 ATCTCCTATACGAGGAGTGTCGTTAAAAATGGTGATTTTAATAATGGATTAGCA 311: Qy 3115 TGCTGGAATGTAAAAGGGCATGTAGATGTACAACAAGAGCCATCACCGTTCTGTCTTGTT 317: Db 3112 TGCTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCTTGTT 317:	3175 ATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGCGTCGCTTT 3 3172 ATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGCTAT 3	3235 ATCCTCGTGTCACAGCGTACAAAGAGGGGATATGGAGAGGGTTGTGTAACGATCCATGAA 3 3232 ATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGAGGTTGTGTAACGATCCATGAA 3	OY 3295 ATCGROACCATACAGACTAAAATTTAAAACTGTAAGGAAGTGTATCCA 335- Db 3292 ATCGAGAACAGTACAGACGAACTTAAAATTTAAAAACTGTGAAGGAAG
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TTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAAAGGGAAGGGAAGTTTATTGTA 3651
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                                                                                                             CCGACTTATGAAGAAAGAAACGTATACAGATGTACGAAGAGATAATCATGTGAGAAATGTGAC
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delta-B.

The sequence encodes a B. thuringiensis Lepidopteran-active endotoxin, crystal protein CryET54. The Lepidopteran-active

Claim 17; Page 168-169; 173pp; English.

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thuringiensis delta-endotoxin polypeptides may be used as compositions that are applied to plant crops to protect them from insect damage. The polynucleotides may be used in the production of transgenic plants that express the insecticidal polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicotyledonous plants may be protected in this way, for example corn, wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato, tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry, fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree cell. A wide range of finsects (e.g. gypsy moth, looper, tobacco budworm, cotton leaf perforator and spruce budworm) may be affected by application of the insecticidal polypeptides (full details given in specification). Note: The present sequence does not have a cryET number assigned to any Seq.ID number, the indexer has matched the spare sequence to the spare cryET number, which may be incorrect
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1855 AGTATAAGTAATGCAGGTAGACAACGTTTCACTTTGATAAATTGAATTCATTC	1915 AFTACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGGGGTGAATGCT 1974 	1975 CTGTTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATAGAT 2034 	2035 CAAGTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAGAGAGAA 2094 	2095 TTACTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAA	H-H	2215 TTCACATCTATCCATGAACAATCTGAACATGGATGGGGGAAGTGAGAACATTACAATC 2274 [2275 CAGGAAGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGACTTTTAATGAG 2334 	2335 TGTTATCCGACGTATTTATATCAAAAATAGGAGGGCGGAATTAAAAGCTTATACTCGC 2394 	2395 TACCAATTAAGAGGGTATATTGAAGATACTCAAGATTTAGAGATATTTGATTCGTTAT 2454 	2455 AATGCGAAACATGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCAGTT 2514 [2515 GAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACTTTTGAATGGAAT 2574 	2575 CCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAATGTGCGCATCATTCCCATCATTTC 2634 		2695 TTCAAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAG 2754 	2755 AAACCATTATTAGGAGAGCACTGTCTCGTGTGAAGAGAGGAGAAAAATGGAGAGA 2814 	2815 AAACGTGAAAACTACAATTGGAAACAAAACGGGTATATACAGAGGCAAAGAAGCTGTG 2874 	2875 GATGCTTTATTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTGGCATG 2934
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/product= "CrylB"
/note= "insecticidal crystal protoxin; Met initiator
codon is TTG"
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                                                                                                                                                                                                                                                                                                                                                         Query Match 84.9%; Score 3132; DB 2; Length 4074; Best Local Similarity 91.1%; Pred. No. 0; Matches 3372; Conservative 0; Mismatches 300; Indels 30.
                                                                                                                                                                                                                                                                                                                                    Sequence 4074 BP; 1376 A; 687 C; 881 G; 1130 T; 0 U; 0 Other;
                                                                                                                                                                                                              to control or combat Ostrinia - 1 gene/protein for crop prevention.
                                                                                                                                                                                                                                             Claim 1; Page 11-18; 38pp; English.
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P-PSDB; AAR50955.
                                                                                      19-AUG-1992;
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                                           EP589110-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insecticidal crystal protein; ICP; cryIB; Ostrinea nubilalis;
European corn borer; Lepidoptera; Pyralidae; toxin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis CryIB insecticidal protoxin gene.
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(revised)
(first entry)
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1911 TITGGACCAGARAGAGTAACTGTTAACGACCATTAACACAGAGTATCGTAAAT 1910 1811 GCTTATGCTGCTTCAACAATTTTAACACATTTCACAGAGTATCCGAGGTATTTT 174 1811 GCTTATGCTGCTTCAACAATTTTAACACATTTCACAGAGTATCCGAGGTATTTAACAATTTTAACACAATTTCACAGAGTATTTAACACAATTTCACAGAATTTCAACAATTTCACAACAATTTCACAACAATTTCACAACA
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11 THATTANGGRANATAGCCTCAAGCTCCAAATTATATATATATGAGGGCCAC 66 7.17 CHITTICITICITICITICITICITICITICITICITICI

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cryE14; cryE75; Lepidoptera; lepidopteran insect; insecticidal; toxin;
insecticidal crystal protein; ICP; ds.
                                                                                                                                                                                                     Isolated cryET4 gene and Bacillus thuringiensis cultures transformed this gene - used in compsns. against lepidopteran insects.
                                                                               /*tag= b
/note= "oligonucleotide WD162,
                                                   Location/Qualifiers
67. 3756
/*tag= a
/253. .272
                                                                                                                                                                                                                         Disclosure; Col 29-38; 51pp; English.
                                                                                                                                                                     Jany CS, Donovan WP,
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                                      Bacillus thuringiensis
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       gene.
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B. thuringlensis strain EG5847 exhibits insecticidal activity against lepidopteran insects. Two novel toxin genes from B. thuringlensis EG5847 designated cryET5 produce insecticidal proteins with activity against a broad spectrum of lepidopteran insects. The gene sequences are given in AAQ64111-12
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                                                                                                                                                                                                               Length 3932;
                                                                                                                                                          Sequence 3932 BP; 1347 A; 650 C; 840 G; 1095 T; 0 U; 0 Other;
                                                                                                                                                                                                       Query Match 72.9%; Score 2687.2; DB 2; Length Best Local Similarity 83.5%; Pred. No. 0; Matches 3088; Conservative 0; Mismatches 593; Indels
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1492 ACCATTAGTTCAGATAGCATAACACAATACCATTGGTAAAATCATTCAACCTTAATTCA 1551 	1552 GGTACCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGATATAATCCGAACTAACGTT 1611 	1612 AATGGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGC 1671 	1672 GTGAGAGTTCGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGAGGGGGT 1731 	1732 ACTACTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAA 1791 	1792 TCATTTAGATTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGA 1851 	1852 ATAAGTATAAGGAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATT 1911 	1912 CCAATTACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGCGCAAGAGGCGGTGAAT 1971 	1972 GCTCTGTTTACTAATACGAATCCAAGAATGATGAAAACAGATGTGACAGATTATCATATT 2031 	2032 GATCAAGTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAGGGA 2091 	2092 GAATTACTTGAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAA	2152 GATCCAAACTTCACATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCG 2211	2212 AATTTCACATCTATCCATGAACAATCTGAACATGGATGGTGGGAGGAAGTGGAACATTACA 2271	2272 ATCCAGGAAGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAAT 2331 	2332 GAGTGTTATCCGACGTATTTATATCAAAAATAGGAGAGTCGGAATTAAAAGCTTATACT 2391 	2392 CGCTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATTTGATTCGT 2451 	2452 TATAATGCGAAACATGGATGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTCA 2511	2512 GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCACATTTTGAATGG 2571
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This invention describes novel transformed plants containing Bacillus thuringiensis strain EGS847 insecticidal crystal protein genes cryET4 or cryET5. cryET4 and cryET5 are novel toxin genes which produce insecticidal proteins with activity against a broad spectrum of insects of the order Lepidoptera. This sequence encodes the cryET5 protein described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 TIGACTICAAATAGGAAAAATGAGAATGAAATTATAAAATGCTITATCGATTCCAACGGTA
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Donovan WP;
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/note= "No ATG start
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67. .3756
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   AATCCTGATCTAGATTGTTCCTGCAGAGATGGAGAAAAATGTGCGCATCATTCCCATCAT
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361	CTTGCTCGAFTTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT	ò	1432 CAATCTAGGG
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781	ACGITAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840	දු අ	
64.	ACCITACOSOS ATTACATOTADA CARACTATACO CACTATACA CACTATACA ATTACA A	à	1912 CCAATTACTG
907	ATCAATACGAGTGCTCAGTTAACAAGAAATTTATACAAGATCGAATTGGGAGAAGAAT	qa	1981 CCAGCAGAGG
901	GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTTTCCGCT	රි ස්	1972 GCTCTGTTTA
196		3 8	2032 GATCAAGTAT
1027	ATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTTTTTTT	qq	
1015	TITAGCACTICACCATGCAGAGGAGTACTACACATAGCATACTACTACTACTACTACTACTACTACTACTACTACTA	à	2092 GAATTACTTG
1087	TACAGTGCATCAAGCCGTTGGAGTAGCACTCAACATATGAATTATTGGGTGGG	QQ	
1075		ે દે	2152 GATCCAAACT
1147	CTTAACTTCCGCCCAATAGGAGGACATTAAATACCTCAACACAGACTTACTAATAAT 1206	g 8	2221 GAICCAAACI
1132	ACTICIATIBATICETGRAAGATTATCATTCTTCTCGAGACGTATATTGGACTGAATCA	À 6	2212 AATTTCACAT 2281 AACTTCCCT
1207	ACTICAATTAATCCTGTAACATTACAGTTTACGTCTCGAGACGTTTATAGAACAGAATCA	ò	2272 ATCCAGGAAG
1267	ATTECAGGGGACAATTTACTATTTACTTACTGGTGAATGGGGGTACCTTTGGGCT	Q	2341 ATTCAGGAAG
1252		ð í	2332 GAGTGTTATC
1321		qq ·	2401 GAGTGTTATC

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1620 2100 1431 1500 1491 1551 1611 1671 rrirggagararacarraaararraargreccarrarcccaaagararcgc 1740 1860 acrigcaggartragractccrrrraartrrrrraartgcccaaagcacatrc 1920 1971 2040 2031 2091 2160 2151 2220 2211 2280 2340 2331 2400 2271 CCGACGATTTATATCAAAAATAGGAGAGTCGGAATTAAAAGCTTATACT 2391 GATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAA 1791 GGGAGTTGGGATTCAATTTTGATTCAGAAACTGAAATTACCACCAGAAACA CCAAATTATGAATCATATAGGTTATCTCACATAGGGCTCATTTCA TTTGCAGAATTTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGA TCACCTGGGCTTCAATTAAAAGATTCAGAAACTGAATTACCACCAGAAACA GTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGGGGTATCGC ATTGGTAATTTCTCAAGAACTATGAATAGGGGGGGATAATTTAGAATATAGA GCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAAT TTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATCG TCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACA

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3532 GACAGAGGGTATGTGAATTATCCACCACTACCAGCTGGTTATATGACAAAAGAATTAGAA
                                                                                                         3601 GACAGAGGGTATGTGAATTATCCACCAGTACCAGCTGGTTATGTGACAAAAAAATTAGAA
                                                                                                                                                                            3592 TACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGAGAAAACGGAAGGGAAGTTTATT
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Ostrinia nubilalis; Pseudoplusia includens; Plutella xylostella;
Spodoptera exigua; Spodoptera frugiperda; Trichoplusia ni; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lepidopteran toxic Bacillus thuringiensis crystal protein - useful control Lepidopteran pests.
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67. .3756
/*tag= a
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IGAAAGGGTACTGCTAACTATAGTCAA 1311 TTCAGAAACTGAATTACCACCAGAAACA 1371 ||||||||||||||||||||||||||||| TTCAGAAACTGAATTACCACCAGAAACA 1440 ATTGGTAAAATCATTCAACCTTAATTCA 1551 BABARCAGATGTGACAGATTATCATATT 2031 rGAACCTATTCATGGTGTCCCTACTGT 1251 TAGGTTATCTCACATAGGGCTCATTTCA 1431 PATAATACATCATTACAGCGGTATCGC 1671 ACAATTTTCACGAGAATTAATGGAACC 1800 AGTGCAAATGAGTCTTTGACATCTCAA 1791 SAATAGGGGGATAATTTAGAATATAGA 1860 PAGTGCATCTGGCAGTCAAACTGCTGGA 1851 raatritraaargcccaaagcacarrc 1920 GTTTCACTTTGATAAATTGAATTCATT 1911 GATGAATTCTGCTTAGATGAAAGAGA 2091 ACTCAGTGATGAAGAAACTTACTCCAA 2151 AGACTTCATATCTACTAATGAGCAATCG 2211 TCTCGAGACGTATATTGGACTGAATCA 1191 AGGAGGGATATAATCCGAACTAACGTT 1611 SGTCCTGAGGGTAACTGTCGGAGGGAGT 1731

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This sequence represents the cryETS gene of Bacillus thuringiensis (B.t.) isolate BCS5847. B.t. produces inclusions during sporulation which include insecticidal crystal proteins (ICP). ICP toxins are active in insects only after ingestion. Once ingested, the toxic components disrupt the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding insecticidal protein - useful
                                                                                                                                                                                                                                                                                  3661 TACTTCCCAGAAACAGATACAGTATGGATTGAGATTGAGAAACGGAAAGGAAAGTTTATT
                                             CCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGTATGTAAT
                                                                     3421 CCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGCAGCATGTAAT
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toxin; CryI protein; lepidopteran insect; insecticide; d
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midgut cells, resulting in cessation of feeding, and eventually death. The CryI proteins produced by B.t. are active against lepidopteran insects. The protein encoded by this sequence, and the CryET4 protein (see AAW17700) belong to the CryI family of ICPs. This sequence can be used to transform bacteria, which are useful as insecticides against a wide range of lepidopteran pests, and can be applied to crops, soil and seeds. The encoded protein, or especially its toxic N terminal region, can be expressed in plants, to provide protection against lepidopteran pests. This sequence, or its fragments, can also be used to isolate other similar genes. (Updated on 25-MAR-2003 to correct PP field.) 120 186 180 246 240 306 480 126 300 366 360 426 420 486 546 540 909 600 9 GTAGCCGAGGTGAACAATATTGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATA TTGACTTCAAATAGGAAAATGAAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA TCGAATCATTCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGT ATAGCCGAGGGAATAATATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATT AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGCTGGACAAATAGCTAGT TTTTATAGTTTTCTTGTTGGTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTC CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCA CTGGAACATGTAGACAACTTATAAGACAACAAGTAACAGAAAATACTAGGAATACGGCT CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT ATTGCTCGATTAGAAGGTCTAGGAAGAGGCTATAGATCTTACCAGCAGGCTCTTGAAACT TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATAGCC TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA TTAGAACTTGACATTACTACTGCTATACCGCTTTTCAGAATACGAATGAAGAACTTCCA TTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCT Gaps Length 3934; 15, Sequence 3934 BP; 1347 A; 650 C; 841 G; 1096 T; 0 U; 0 Other; 0; Mismatches 593; Indels DB 2; Score 2687.2; Pred. No. 0; Query Match
Best Local Similarity 83.5%;
Matches 3088; Conservative 67 61 127 121 181 247 301 427 187 241 307 367 547 361 421 487 481 541 8899999999988 셤 g සු 8 6 8 6 6 6 6 6 6 6 ð ઠે ઠે ద ઠ 8 8

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                                                                                                      CryET4; Bacillus thuringiensis strain EG5847; crystal toxin; CryET5; Lepidoptera; Helicoverpa zea; resistant strain; Plutella xylostella; Spodoptera exigua; S. frugiperda; S. frugiperda; Trichoplusia ni; ds.
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                                                                                                                                                                                                                                                                                                                 The present sequence encodes a CryET5 protein. The protein is isolated from a new strain of Bacillus thuringiensis (B.t.), strain EGS847 (NRL 1-2110). EG5847 contains two new crystal toxin genes (cryET4 and cryET5) that produce proteins active against Lepidoptera. CryET4 is more active than CryIA(a) against Helicoverpa zea, resistant-strains of Plutella active active than CryIB against Efrugiperda, while CryET5 is more active than CryIB against S. frugiperda and Trichoplusia ni (and both are active against additional insect species)
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                                                                                                                                                                                                         New strains EG5847 and EG10368 of Bacillus thuringiensis - producing crystal toxins active against Lepidoptera, particularly Helicoverpa ? Plutella xylostella and spodoptera species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3934 BP; 1348 A; 650 C; 840 G; 1096 T; 0 U; 0 Other;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                   Example 2; Fig 2A-J; 49pp; English
           93US-00100709.
93US-00176865.
95US-00474038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
72.9%;
Best Local Similarity 83.5%;
Matches 3088; Conservative
                                                                                                                     Ë
                                                                                                                     Gonzalez
                                                                                                                                                        WPI; 1999-094915/08
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Best Local Similarity
                                                                                                                                                                         P-PSDB; AAW87633.
                                                                                (ECOG-) ECOGEN
           29-JUL-1993;
30-DEC-1993;
07-JUN-1995;
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                      gene;
           oteran insect pest; transgenic plant;
infestation resistance; monocot; dicot; crylBb;
gene therapy
                                                                                                                         /note= "No start or stop codon"
                                                                                                   "B thuringiensis
insecticidal protein; plant; pesticide;
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                                                               Location/Qualifiers
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                                          Bacillus thuringiensis.
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(ROMA/) ROMANO C P.
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GACAGAGGTATGTGAATTATCCACCAGTACCAGCTGGTTATGTGACAAAAGAATTAGAA 3594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hybrid Bacillus thuringiensis hybrid toxins comprising structural domains derived from at least 2 different crystal proteins, such as Crylla and CrylBa, and having insecticidal activity, useful for combating
                                                                                                                                                                                                        Crystal protein; Crylla; CrylBa; moth; butterfly; Colorado potato beetle; ds; mutant.
                              TACTTCCCAGAAACCGATAAGGTATGGATTGGAGAAACGGAAGGGAAGTTTATT
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                                                                                                                                                                                     Bacillus thuringiensis DNA encoding partial mutant CrylBa
                                                                    (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD
                                                          GTAGACAGCGTGGAATTACTCCTTATGGAGGAA 3684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAATATATAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGAACTIGATITITCITAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATIGATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTGAGAGATGCCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCAATTCCGTAGAGATCTAA
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                                                                    TGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTAT
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                                     Gaps
                                   81,
   Length 3627;
                                  Indels
                                                                                              TGACTTCAAATAGGAAAATGAGAATGAAATTATAAAT
 DB 4;
                                   533;
71.3%; Score 2630.2;
83.4%; Pred. No. 0;
ive 0; Mismatches
                Best Local Similarity 53.4
Matches 3081; Conservative
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CCGRGAMACTCANGACACCACCTCACTGATCACCTACTCACTACTCACACTCCACACACCACCACCAC
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1022 CITCATCACCANTGGACTACTACCACATACACTACTCACCCCCCCCCC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insecticidal agent; hybrid toxin; CrylCa; CrylBa; BBCL5; insect control; pest control; crop; insect resistant plant; transgenic plant;
                                                                                                                                                                                               3173 TCCTTCGTGTCACAGCATATAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCATGAGA
                                                                                                                                                                                                                                                                                                                                                                                      3410 ATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                    3353 CTTCTCGTAATCAAGGATATGACGAAGCCTATGGTAATAACCCTTCCGTACCAGCTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3470 ACAAACCGACTTATGAAGAAGAACGTATACAGATGTACGAAGAGATAATCATTGTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3530 ATGACAGAGGTATGTGAATTATCCACCACTACCAGCTGTTATATGACAAAAGAATTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3473 CTAACAGAGGCTATGGGGATTACACACCACTACGGCTGGTTATGTAACAAAGGATTTAG
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                                                    TCCTCCGTGTCACAGGCGTACAAGAGGGATATGGAGAGGGTTGTGTAACGATCCATGAAA
                                                                                                                                                         3296 TCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCAA
                                                                                                                                                                                                                                                                             3356 CGGATACAGGAACGTGTAATGATTATACTGCACCCAAGGTACAGCAGTATGT----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. thuringiensis CrylBa/CrylCa (BBC15) hybrid insecticidal toxin DNA.
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/product= "BBC15"
/note= "This sequence does not contain a stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .3663
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS00422 standard; DNA; 3663 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crystal protein; mutant; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis.
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P-PSDB; AAU00421.
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The present sequence encodes for 1 of 3 novel hybrid insecticidal toxins (AAU00419-AAU00422) and is designated BBCI5. BBCI5 comprises domains I cand II from the Crylae toxin at the Crylae and Crylca toxin at the Crylae and Crylca toxin domains I corresponds to PFCI residues 446-454. In the 1221 amino acid FFCI hybrid corresponds to PFCI residues 446-454. In the 1221 amino acid BBCI3 and BBCI5 hybrid sequences, the juncture between the CrylBa and CrylCa toxin commains is residues 482-488 in the BBCI3 hybrid, and residues 491-494 in the BBCI5 hybrid. The hybrid toxins are useful for controlling and in vivo recombination. The hybrid toxins are useful for controlling and in vivo recombination. The hybrid toxins are useful for controlling and in vivo residue to be the two propers of the BBCI5 hybrid sylostella (diamondback moth), Ostrinia nubilalis insect such as Spodoptera frugiperda (fall armyworm), and Heliothis virescens (tobacco budworm) which are major causes of common to bore?), Spodoptera frugiperda (fall armyworm), and Heliothis virescens (tobacco budworm) which are major causes of cogramate plant by introducing the nucleotide sequence into the plant to preferably a transgenic plant. The nucleotide sequence into the plant corresponding the nucleotide sequence sequence used as an insecticidal agent. Baculoviruses engineered to coxin produced used as an insecticidal agent. Baculoviruses engineered to coxin produced used as an insecticidal agent. Baculoviruses engineered to infect insects in vivo resulting in their death. The hybrid toxins have a companient toxins alone toxin can be used to greater toxicity level than either of their parent toxins alone
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                 Novel hybrid insecticidal toxin useful for controlling insects such as Spodoptera exigua and Plutella xylostella, comprises domains I and II from CrylF or CrylB toxin joined to domain III from CrylC toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 CGAATCATTCCGCACAAATGGATCTATTACCAGATGCTCGTATTGAGGATAGCTTGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 TAGCCGAGGGGAACAATATCGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 TTTATAGTTTTCTTGTTGAATTATGGCCCCGCGGCAGAGATCAGTGGGAAATTTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCTCGATTACAAGGTTTAGGAGATTCCTTCAGAGCCTATCAACAGTCACTTGAAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2544.4; DB 4; Length 3663;
Pred. No. 0;
0; Mismatches 546; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3663 BP; 1190 A; 650 C; 832 G; 991 T; 0 U; 0 Other;
                                                                                                      88-89; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.0%;
Best Local Similarity 82.1%;
Matches 3065; Conservative 0
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2630 CAGACTTAAATGAGGACTTAGGTGTATGGGTGATATTCAAGATTAAGACGCAAGATGGCC 2689
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                                                                              2690 Argchagacraggaarcragagrircrcgaagagaaccarrarragggaagcacrag
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                                                                                                                                                         TTTTTGAAGAATTAGAAGGTCGCATTATCACTGCAATCTCCCTATACGATGCGAGAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3431 AGGATGCATATGAAGTTGATACTACAGCATCTGTTAATTACAAACCGACTTATGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3551 ATCCACCACTACCAGCTGGTTATATGACAAAGAATTAGAATACTTCCCAGAAACCGATA
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The present sequence encodes for 1 of 3 novel hybrid insecticidal toxins (AAU00419-AAU00422) and is designated BBC13. BBC13 comprises domains I and I from the Cryba toxin at the N-terminus joined to domain III from CrylCa toxin at the C-terminus. In the 1186 amino acid FFC1 hybrid corresponds to FFC1 residues 446-454. In the 1221 amino acid BBC13 and BBC15 hybrid sequences, the juncture between the CrylCa toxin domains corresponds to FFC1 residues 446-454. In the 1221 amino acid BBC13 and BBC15 hybrid sequences, the juncture between the CrylCa toxin domains is residues 482-488 in the BBC13 hybrid, and residues 491-494 in domains is residues 482-488 in the BBC13 hybrid, and residues 491-494 in corresponds to the hybrid toxins are constructed by cloning and in insect such as Spodoptera exigua (beet armyworm), Manduca sexta (tobacco hornworm), Plutella xylostella (diamondback moth), Ostrinia nubilalis (Butchis virescens (tobacco budowrm) which are major causes of sequences encoding the hybrid toxins are useful for producing an insectrespect corresponds to the plant to resistant plant by introducing the nucleotide sequence into the plant preferably a transgenic plant. The nucleotide sequence into the plant corresponds in miscrocorganisms such as a virus, bacterium and fungus and the expressed in microorganisms such as a virus, bacterium and fungus and the coxin produced used as an insecticide agent. The hybrid toxin can be used to infect insects in vivo resulting in their death. The hybrid toxins have a cinfect insects in vivo resulting in their death. The hybrid toxins have a cinfect insects in vivo resulting in their death.
                                                                                                                                                                    control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel hybrid insecticidal toxin useful for controlling insects such as Spodoptera exigua and Plutella xylostella, comprises domains I and II from CrylF or CrylB toxin joined to domain III from CrylC toxin.
                                                                                                                       B. thuringiensis CrylBa/CrylCa (BBC13) hybrid insecticidal toxin DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "This sequence does not contain a stop codon"
                                                                                                                                                                  CrylBa; BBC13; insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infect insects in vivo resulting in their death. The hybrid tox:
greater toxicity level than either of their parent toxins alone
                                                                                                                                                            Insecticidal agent; hybrid toxin; CrylCa; CrylBa; BBCl3; inse
pest control; crop; insect resistant plant; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; 828 G; 992 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYNG-) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                           product= "BBC13"
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                                                                                                                                                                                                         crystal protein; mutant; ds.
                                                                                (first entry)
                                                                                                                                                                                                                                                Bacillus thuringiensis.
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P-PSDB; AAU00420.
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                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                               Key
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7;

Gaps

548;

68.9%; Score 2541.2; 82.0%; Pred. No. 0; ive 0; Mismatches

Best Local Similarity 82.0 Matches 3063; Conservative

Query Match

DB 4; Length 3663; Indels 123;

11.2 ATTCCTOTATA ANTINCTICAL COCCATOR CONTRICATOR 1.11 1.
6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8
2 TRACTICAMINGGAMMITGAGAIGAMTHAINAITH CONTINUED CONTINUE

Qy 3257 AAGAGGGATATGGAGAGGGTTGTGAACGATCCATGAAATCGAGAACAACAACAACAACAACAACAACAACAACAACAAC	Search completed: November 21, 2004, 09:24:38 Job time :-1588 secs		
2144 AGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGGATCAATAGAC 2203 2180 AACCAGACTTCATATCTACTAATGAGCAATCGAATTTCACATCTATCCATGACAATCTG 2239 2204 AACCAGACTTCATATCTACTAATGAGCAATTCACATCTATCCATGAACAATCTG 2239 2210 AACCAGACTGAGAGAAGTAACAATTAACAATCCAGAAATTAATAATCAAG 2299 2211GGTGGCTGGAGAAGTAATTAACAATTAACAAGAGAGAATTAATT	2660 CAGACTIGCATGACATTCTAGGCTGTGCGTGTTTCAAGATTAAGACGCAGGAAGGC 2719 2630 CAGACTTAAATGAGGCTTAGGCTGTATTCAAGATTAAGACGCAAGATGGCC 2689 2720 ATGCAAGACTTAGGGTGTTTTTTGAAGACCATTATTAGGAGAACAGTGC 2779 2630 ATGCAAGACTTAGGGATTTTTTTGAAGAACCATTATTAGGAGAACACTGT 2779 2690 ATGCAAGACTAGGAATTTTTTTTTTTTTTTTTTTTTTTT	3080 TCGTTAAAAATGGTGATTTTAATAATGGATTAGCATGCTGGAATGTAAAAGGCGTGTAG 3139 1050 TCATTAAAAATGGCGATTTCAATAATGGCTTATTATGCTGGAACGTGAAAGGTCATGTAG 3109 3140 ATGTACAACAGAGCCATCACGTTCTGCTTATTCCCAGAATGGGAAGGTCATGTAG 3109 3110 ATGTAGAACAGAGCCATCACGTTCTGTTATCCCAGAATGGGAAGGAAG	3197 TGTCACAGGGGTTCGCGTCTGTCCGGGGCGTGCTATATCCTCCGTGTCACAGCGTACA 3256

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Sequence 37, Appli Sequence 7, Appli Sequence 5, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli
                                                                                                                                                                                                                                        November 21, 2004, 08:58:21; Search time 321 Seconds (without alignments) 8164.108 Million cell updates/sec
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Sequence 22, P
Sequence 22, P
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-951-803-5
US-08-170-690-1
US-08-170-865-3
US-08-176-865-3
US-08-177-06-3
US-08-913-340-3
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US-08-434-813-1

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US-08-459-5948A-6

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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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		GENERAL INFORMATION:	DRMAT	ION:											
			Baum	, g	Baum, James A.										
		CANT		yan,	willi	E	G								
		ICANT:	611	mer,	Amy J.		:								
		ICANT:	Rup	ar, l	Mark J.	4			Ç						
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		FILE REFERENCE: MECO201	ENCE:	MEG	0201 MIMBED	Ě	00/2	155/	4000						
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		NUMBER OF SEQ ID NOS: 63 SOFTWARE: PatentIn version 3	SEQ I.	D NO.	S: 63 version	3.0									
	ഗു	Q ID NO 37	52												
		TYPE: DNA	:												
		ORGANISM: Bacillus thuringiensi Frature.	Baci	llus	thurin	gie	nsie								
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	, LOC US-09-6	LOCATION: (1)(3687) .09-661-322A-37	(1). 1-37	. (36	87)										
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Sequence 7, Application US/08448170
Patent No. 5723758
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: B.c. Psibsc2, Active Against Lepidopteran Pests, and Genes
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/448,170
FILING DATE:
CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/448,170
FILING DATE:
CLASSIFICATION: 424
FRIOR APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION 1424
FRIOR APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: M/S 102D.C1
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ 1D NO: 7: SEQUIRCE CHARACTERISTICS:
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                                                                        ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
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Matches 3449; Conservative
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                                                                                                                                                                                      Score 3266.6;
Pred. No. 0;
0; Mismatches
TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-961-803-5
                                                                                                                                                                                    88.6%;
llarity 93.4%;
Conservative C
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Best Local Similarity
Matches 3449; Conserv
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                                      GTAAATATGGCAAGTATGAATTGGTATAATAATAATGCACCTTCGTTCTCTGCCATAGAG
                                                                          ACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATTTTTAGC
                                                                                         GCTGCGGCTATCCGAAGCCCGCATCTACTTGATTTTCTAGAACAACTTACAATTTTTAGC
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                                                                                         CryIB is toxic (among others)"
                                                                                                                                                                    Indels
                                                                                                                                           DB 1;
                                                                                                                                                                 299;
                                                                                                                                         Score 3133.6;
Pred. No. 0;
0; Mismatches
                                                               MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: entomocidus HD 110
FEATURE:
                                                                                                                                         Query Match
Best Local Similarity 91.1%;
Matches 3373; Conservative
                                                                                                      ;
US-08-377-690-1
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US-00-100-709-3

Sequence 3, Application US/08100709

Patent No. 5322687

GENERAL INFORMATION:

APPLICANT: Donovan, William P.

APPLICANT: Tan, Yuping

APPLICANT: Tan, Christine S.

APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: BACILLUS THURINGIENSIS CTYETA AND CTYE

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPI

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STATE: Pennsylvania

CONTRY: U.S.A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
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                                                                                                                                                                                                                      72.9%; Score 2687.2;
83.5%; Pred. No. 0;
tive 0; Mismatches
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: EGOLF, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-75-1590
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPPLOGY: circular
                                                                                                                                MOLECULE TYPE: DNA (genomic)
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2253..2272
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LOCATION:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Plopyy disk

COMPUTER: IMP PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,865

FILING DATE: 30-DEC-1993

CLASSIFICATION: 435

PRICH APPLICATION NAMBER: US 08/100,709

FILING DATE: 29-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Egolf, Christopher

REFEISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 27633

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LEMGTH: 3934 base pairs
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              GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tan, Yuping

APPLICANT: Tan, Yuping

APPLICANT: Jany, Christine S.

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

ADDRESSEE: Nadel
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible

COMPUTER PER Floppy disk

TELING DATE: 07-010-1995

FILING DATE: 07-010-1993

ATTORNEY AGENT INFORMATION:

NAME: EGGIE, Christopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

TELECOMMUNICATION NUMBER: 7205-49

TELECOMMUNICATION NUMBER: 7205-49

TELECOMMUNICATION NUMBER: 7205-49

TELECOMMUNICATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

TELECOMMUNICATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 27633

REFERENCE/DOCKET NUMBER: 27633

TELECOMMUNICATION NUMBER: 27633
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83.5%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                   STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
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2253..2272
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STRANDEDNESS: double
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Matches 3088; Conserv
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FEATURE:
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Sequence 3, Application US/08779046
Sequence 3, Application US/08779046
SENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
ADDRESSES: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSES: Nadel.
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                 TTGACTTCAAATAGGAAAAATGAGAATGAAATTATAAATGCTTTATCGATTCCAGCTGTA
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Pred. No. 0;
0; Mismatches 593; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

SECTIVED TO BATE: D6-D0S/MS-D0S

FILING DATE: 06-JAN-1997

CLASSIFICATION NUMBER: U8/08/779,046

FILING DATE: 29-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: EGGIL, Christopher:

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                        GTAGATAGCGTGGAACTACTCCTCATGGAAGAATAG 3756
                                                                                                                                               GIAGACAGCGTGGAATTACTCCTTATGGAGGAATAG 3687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
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MOLECULE TYPE: DNA (genomic)
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ilarity 83.5%;
Conservative (
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2253..2272
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STRANDEDNESS: double
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Matches 3088;
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US-08-779-046-3
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72.9%;
Best Local Similarity 83.5%;
Matches 3088; Conservative
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NAME/KEY:
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Patent No. 594268

GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Gonzalaz Jr., Ose M.
TITLE OF INVENTION: DACILLUS THURINGIENSIS cryET4 AND cryET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CTTV. Dhiladanki.
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CITY: Philadelphia
STATE: Pennsylvania
STATE: Pennsylvania
CONNTRY: U.S.A.

ZIP: 19103

COMPUTER: ENDABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-JUN-1997
CLASSIFICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-193
APPLICATION NUMBER: 20-JUS-193
ATTORNEY/ASENTIN NUMBER: 27-33
REFERENCE/DOCKET NUMBER: 2763
TELECOMMUNICATION INFORMATION:
MANE: EGOIF, CALLACTERISTICS:
TELECOMMUNICATION INFORMATION:
MANE: MA
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Pred. No. 0;
0; Mismatches 861; Indels 117;
                                                                                                                                                                                                                                                                                                               STRAIN: alzawai
INDIVIDUAL ISOLATE: PS81A2
INMEDIATE SOURCE:
LIBRARY: Lambdagem - 11 (tm) Library of August Sick
CLONE: 81A2
                                                                                                                                                                                                                                                                                             Bacillus thuringiensis
                    TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3522 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTT-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.6%;
Best Local Similarity 71.9%;
Matches 2497; Conservative (
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-040-751-4
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APPLICANT: Sick, August J
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes Encoding No. TITLE OF INVENTION: Lepidopteran-active Toxins
NUMBER OF SUVENION: 1. Lepidopteran-active Toxins
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
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                                                      1181 ACATGTTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCATCGTTCTGACCTT
                                                                                                                                                                                             TATATCCTCCGTGTCACAGCGTACAAGAGGATATGGAGAGTTGTGTACGATCCAT
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     GCATGCTGGAATGTAAAAGGGCATGTAGAACAACAGAGCCATCACGGTTCTGTCCTT
                                                                                                     GTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGC
                                                                                                                                                 GTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCCGGGGCGTGGC
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,751
FILING DATE: 19930329
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COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5407825
GENERAL INFORMATION:
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CLASSIFICATION:
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US-08-040-751-4
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Pred. No. 0;
0; Mismatches 861; Indels 117;
                                                                                                                                                                                                                                                     STRAIN: aizawai
INDIVIDUAL ISOLATE: PS81A2
IMMEDIATE SOURCE:
LIBBIARY: Lambdagem - 11 (tm) Library of August Sick
CLONE: 81A2
                                                                                                                                                                                                                                    ORGANISM: Bacillus thuringiensis
                                                                                 TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
TELEFAX: (904)372-5800
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3522 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.9%;
Matches 2497; Conservative
                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                            US-08-291-368-1
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    TTCTGTCCTTGTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCC
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Sequence 1. Application US/08291368

GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5686069el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Galnesville
STREET: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTEY: US

ZIP: 32606

COMPUTER READBLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/291,368

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/597,607

FILING DATE: 15-OCT-90

CLASSIFICATION: 536

CLASSIFICATION: 536
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NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MASO.C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-291-368-1
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Best Local Similarity 71.9%; Pred. No. 0;
Matches 2497; Conservative 0; Mismatches 861; Indels 117; Gaps
                                                                                                                                                                                                                                                                                                         STRAIN: aizawai
INDIVIDUAL ISOLATE: FS81A2
IMMEDIATE SOURCE:
LIBRARY: Lambdagem - 11 (tm) Library of August Sick
CLONE: 81A2
                                                                                                                                                                                                                       HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
INFORMATION: (904)375-8100
TELEFAX: (904)375-8100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3522 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOCY: linear
                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                GGGGCGTGGCTATATCCTCCCGTGTCACAGCGTACAAGAGGGATATGGAGAGGGTTGTGT
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Patent No. 5985267

GENERAL INFORMATION:
APPLICANT: Sick, Jewel M.
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5985267el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STRTE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,190
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,368
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FILING DATE: 15-OCT-90
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MASO.C1
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STRAIN: aizawai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGAGATAATCATTGTGAATATGACAGAGGGTATGTGAATTATCCACCACTACCAGCTGG 3569
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TGGCTTATCATGCTGGAACGTGAAAGGCCATGTAGATGTAGTAGAACAAAACAACCACCG 2987
                                  TTCTGTCCTTGTTATCCCAGAATGGGAAGCAGAAGTGTCACAAGCAGTTCGCGTCTGTCC 3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: STREET ADDRESS: 5501 Oberlin Drive
APPLICANT: STREET ADDRESS: 5501 Oberlin Drive
APPLICANT: STATE/FROYINCE: California
APPLICANT: STATE/FROYINCE: California
APPLICANT: COUNTRY: US
APPLICANT: POSTAL CODE/ZIP: 92121
APPLICANT: PHONE NUMBER: (619) 453-6901
APPLICANT: FAX NUMBER: (619) 453-691
TITLE OF INVENTION: Protein Toxins Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
TITLE OF INVENTION: Protein Toxins Active Against Lepidopteran STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGCGTGGCTATATCCTCCGTGTTACAGCGTACAAAGAGGGATATGGAGAAGGTTGCGT
                                                                                                                                                                         AACGATCCATGAAATCGAGAACAATACAGACGAACTAAAATTTTAAAAACTGTGAAGAAGA
                                                                                                                                                                                                          AACCATCCATGAGATCGAGAACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAAGA
                                                                                                                                                                                                                                                                               GGAAGTGTATCCAACGGATACAGGAACGTGTAATGATTATACTGCACCACCAAGGTACAGC
                                                                                                                                                                                                                                                                                                                   AG-----TATGTAATTCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGA
                                                                                                                                                                                                                                                                                                                                                                                    TACTACAGCATCTGTTAATTACAAACCGACTTATGAAGAAGAAACGTATACAGATGTACG
                                                        GGGGCGTGGCTATATCCTCCGTGTCACAGCGTACAAAGAGGGATATGGAGGGGTTGTGT
                                                                                                                                                                                                                                           GGAAGTGTATCCAACGGATACAGGAACGTGTAATGATTATACTGCACACCAAGGTACAGC
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STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTE: IBM PC compatible
COMPUTE: ASTEM: PC-DOS/MS-DOS
SOCTMARE: PSTEM: Release #1.0, Version #1.
CURBENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9510310 GENERAL INFORMATION:
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APPLICATION NUMBER: 07/597,607
FILING DATE: 15-OCT-90
CLASSIFICATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-10310-1
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Pred. No. 0;
0; Mismatches 861; Indels 117; Gaps
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INMEDIATE SOURCE:
LIBRARY: Lambdagem - 11 (tm) Library of August Sick
CLONE: 81A2
                                          NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFRENCE/DOCKET NUMBER: MASO.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
TELEFAX: (904)372-8800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3522 base pairs
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Best Local Similarity 71.9%;
Matches 2497; Conservative
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: double
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                                                                                         GTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAAGAGTGTTCTTTATAC
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TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES ACTIVE
AGAINST LETPLOPPERAN PESTS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/451,389
FILING DATE: 14-DBC-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-MAY-1989
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Search completed: November 21, 2004, 16:55:54 Job time : 355 secs

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Sequence 22, Appl
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(c) 1993 - 2004 Compugen Ltd.
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7 US-10-809-953-9

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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ALIGNMENTS

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APPLICANT: Mathieu, Eva APPLICANT: Vanneste, Stijn APPLICANT: Vanneste, Stijn APPLICANT: Vanneste, Stijn APPLICANT: Van Rie, Jercen TITLB OF INVENTION: Insecticidal proteins from Bacillus thuringiensis. FILE REFERENCE: NEWBERSUGS: CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-28
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                     Sequence 1, Application US/10614524
Publication No. US20040016020A1
GENERAL INFORMATION:
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SEQ ID NO 1
LENGTH: 3687
                                                                                      APPLICANT: Arnaut, Greta
APPLICANT: Boets, Annemie
APPLICANT: Damme, Nicole
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 13
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; LOCATION: (1)..(3687)
US-10-614-524-1
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Sequence 25, P Sequence 25, Sequence 25,

US-09-916-956A-25 US-09-997-914-25 US-09-837-961-7 US-10-825-751-7 US-09-873-873-25

Sequence 7, Sequence 7,

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Qy 3301 AACAATACAGAACTAAAATTTAAAAACTGTGAAGAAGAGGAAGTGTATCCAACGGAT 3360 Db 3301 AACAATACAGACGAACTAAAATTTAAAAACTGTGAAGAGGAAGTGTATCCAACGGAT 3360 Qy 3361 ACAGGAACGTGAATTATACTGCACCCAAGGTACAGCAGTATGTAATTCCCGTAAT 3420 Db 3361 ACAGGAACGTGAATGATTATACTGCACACCAAGGTACAGCAGTATTAATTA	RESULT 2 US-10-428-961-37 US-10-428-961-37 Sequence 37. Application US/10428961 Publication No. US20030237111A1 GENERAL INFORMATION: APPLICANT: Baum, James A. APPLICANT: Chu, Chih-Rei APPLICANT: Chu, Chih-Rei APPLICANT: Glimer, Amy J. APPLICANT: Rupar, Mark J. APPLICANT: Glimer, Amy J. APPLICANT: Glimer, Amy J. APPLICANT: Applicant Rupar, Mark J. APPLICANT: Glimer, Amy J. APPLICANT: Applicant Rupar. Wark J. APPLICANT: Glimer, Amy J. APPLICANT: Mark J. APPLICANT: Glimer, Amy J. APPLICANT: ON NUMBRR: US/10/428,961 CURRENT APPLICATION NUMBRR: 09/661,322 PRIOR APPLICATION NUMBRR: 60/153,995 PRIOR FILING DATE: 1999-09-15 NUMBER OF SEQ ID NOS: 63 SOFTWARE: Patentin version 3.2 SEQ ID NO 37 LEAGTH: 4173 TYPE: DAA	ORGANISM: Bacillus thuringiensis FRETURE: FRETURE: FRETURE:
2221 TCTATCCATCAACAATCTGAACATGGATGGGGAAGTGAGAACATTACAATCCAGGAA 2280 2221 TCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTACAATCCAGGAA 2280 2221 TCTATCCATGAACAATCTGAACATGGGTGGGGAAGTGAGAACATTAACAACATCCAGGAA 2280 2281 GGAAATGACGTATTTAAAGAGAATTACGTCACACTCACGGGGACTTTTAATGGTGTTAT 2340 2281 GGAAATGACGTATTTAAAAAAAATAAGGAGACTCACCACGGGACTTTTAATGGTGTTAT 2340 2341 CCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTAAAAGCTTATAATCGCTACCAC 2400 [2641 GATATTGATATTGGATGACAGACTTGCATGAGAATCTAGGCGTGTGGGTGCTATTCAAG 2700 2641 GATATTGATATTGCATGCACAGACTTGCATGCACGCGTGTGGGTGCTATTCAAG 2700 2701 ATTAAGACGCAGGAAGCTTGCATGCATGCATCTGGAATTTATTGAAGAAACCA 2760 2701 ATTAAGACGCAGGAAGGTCATGCAAGAATCTGGAATTTATTGAAGAAACCA 2760 2701 ATTAAGACGCAGGAAGGTCATGCAAGAACAGGAAATTATTGAAGAAACCA 2760 2701 ATTAAGAAGACACTGTCTCGTGTGAAGAACAGAAAAAATGAAGAAACCA 2760 2761 TTATTAGGAAAAGACCTGTCTCGTGTGAAGAAGAAGAAAATGAAGAAACAAAC	3001 CCGGGTGTAAATGCGGAAATTTTGAAGATTAGAAGGTCGCATTATCACTGCAATCTCC 3060 3001 CCGGGTGTAAATGCGGAAATTTTTGAAGAATTAGAAGGTCGCATTATCACTGCAATCTCC 3060 3001 CCGGGTGTAAATGCGGAAATTTTTGAAGAGTCGCATTATCACTGCAATCTCC 3060 3001 CTATACGATGCGAGAAATGTCGTTAAAAATGGTGATTTAATAATGGATTAGCATGCTGG 3120 3121 AATGTAAAAGGGCATGTACGTTAAAAATGGTGATTTTAATAATGGATTAGCATGCTGG 3120 3121 AATGTAAAAGGGCATGTACAAAAAAAAGGGCCATCACCGTTCTGTCCTTGTTATCCCA 3180 3121 AATGTAAAAAGGGCATGTACAAAAAAAAGGCCATCACCGTTCTGTCCTTGTTATCCCA 3180 3181 GAATGGGAAGTGTCACAAAGAAGCAGTTCGCGTCGTCTGTCT

1261 TITAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCCTATGAG 1320 	1321 TCACCTGGGCTTCAATTAAAGATTCAGAAACTGAATTACCACCAGAAACAACAAGAACGA 1380 	1381 CCAAATTATGAATCATAGGTTATCTCACATAGGCTCATTTCACAATCTAGG 1440 	1441 GTGCATGTACCAGTATATTCTTGGACGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500	1501 TCAGATAGCATAACCATAGGTAAAATCATTCAACCTTAATTCAGGTACCTCT 1560 	1561 GTAGTCAGTGGCCCAGGATTTACAGGGGGATATAATCCGAACTAACGTTAATGGTAGT 1620 	1621 GTACTAAGTATGGGTCTTAATTTTAATAACATCATTACAGGGGTATCGCGTGAGAGTT 1680 	1681 CGTTATGCTGCTTCTCAAACAATGGTCCTGAGGGTAACTGTCGGAGGAGTACTATT 1740 	1741 GATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCATTTAGA 1800 	1801 TITGCAGAAITICCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860 	1861 AGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCATTC	1921 GCAACCTTCGAAGCAGAATACGATTTAGAAAGGCGCAAAGAGCGCTGAATGCTCTGTTT 1980 	1981 ACTAATACGAATCCAAGAAGATTGAAAACAGATGGACAGATTATCATATTGATCAAGTA 2040 	2041 TCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAGAGAGAG	2101 GAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAAA	2161 TTCACATCCATCAATAAGCAACCAGACTTCATATCTACTAAGCAATGGAATTTCACA 2220 		2281 GGAAATGACGTATTTAAAGAGAATTACGTCACACTACCGGGGACTTTTAATGAGTGTTAT 2340
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Sequence 62, Application US/10428961

Sequence 62, Application US/10428961

Fublication No. US20030237111A1

SERERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chil-Rei

APPLICANT: Chu, Chil-Rei

APPLICANT: Glimer, Amy J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE MECO201-1

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE PATENTING DATE: 2003-05-05

NUMBER OF SEQ ID NOS: 63

SEQ ID NO 62

SEQ ID NO 62
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                    TTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAATGCG
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1435 TCTAGGGTCCANTTACAGGTACCAGCAGCAGCAGTAGTACTACAAATACC 1491 1432 AACACTTCAGATACACACAAAACCATTGGAAACCACACAAATACC 1491 1439 ATTACTCAGATACACACAAACCATTGGAAACCACTTCAACCATTACTACTTCAGTACTACTTCAGTAC
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10 CTAGAACATGTCGAACATTCTTRAAGACACAGAACATTCTGAACATACAGAACATCTGGGGGT 160

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1561 GTAGTCAGTGGCCCAGGATTTACAGGAGGGATATAATCCGAACTAACGTTAATGGTAGT	180 178 185 184	ACTGCAACCTTCGAAGCAGATACGATTTAGAAGGCGCAAGAGGCGCGAAGGCGTGAATGTTCCAGT 190 ACTGCAACCTTCGAAGCAGAATACGATTTAGAAGGCGCGAAGGGCGGTGAATGCTCTG 190 ACTGCAACCTTCGAAGCAGAATTAGAAAAGAGCGCAGAGGCGGTGAATGCTCTG 196 TTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAA 203 TTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAA 203 TTTACTAATACGAATCCAAGAAGATTGAAAACAGATGTGACAGATTATCATATTGATCAA 202	GTATCCAATTTAGTGGCGTGTTTATCGGATGAATTCTGCTTAGATGAAAGAGAGAG	221 220 227 227 226		2398 CAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATTTGATTCGTTATAAT 2457 2386 CAATTAAGAGGTTATATTGAAGATAGTCAAGATTTAGAGATATTTGATTCGTTATAAT 2445 2458 GCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGACGCGCTTTCAGTTGAA 2517 2466 GCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGGCGCTTTCAGTTGAA 2517 2446 GCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCCTATGGCCGCTTTCAGTTGAA 2505	2518 AGCCCAATCGGAAGGTGCGAAACCGAATCGATGCGCACCATTTGAATGGAATCCT 2577 2506 AGCCCAATCGGAAGGTGCGGAACCGAATCGATGGCACCACTTTTGAATGGAATCCT 2565 2578 GATCTAGATTGTTCCTGCAGAGATCGAAAAATGTGCGCCATCATTTCCATCATTTCTCT 2637 [
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406 TGGCTAGAAAACCGTGATGATGCAAGAAGTGTTCTTCATACCCAATATATAGCT 465 481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 540 466 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA 525 541 TTATTAATGGTATATGCTCAAGCTGCAATTTATTATTATGAGAGAGCCTCT 600 526 TTATTAGATGGTATATGCTCAAGCTGCAAATTTATTATTATGAGAGATGCCTCT 585 601 CTTTTTGATGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGAGACCCAA 660 586 CTTTTTGGTAGTAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGAGCCCAA 660 586 CTTTTTGGTAGTAATTTGGGCTTAAATTGAGGAAATTCAACGTTATTATGAGAGCCCAA 660 586 CTTTTTTGGTAGTAATTTGGGCTTAAATTGAGGAAATTCAACGTTATTATGAGAGCCCAA 660		**************************************	961 ACTGCGGTTATCCGAAGCCCGCATCTACTTTCTAGAACAACTTACAATTTTAGC 1020		1201 GTGGTTCTATGGGGAATTTACCTTGACCTATTCATGGTGTCCCTACTGTTAGATTTAAT	1321 TCACCTGGGCTTCAATTAAAAGATTCGGAAATTACCACCAGAACAACAACAGAACGA 1380	

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                                                                                                                                Encoding Pesticidal Toxins
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Pred. No. 0;
0; Mismatches 1084; Indels 156;
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                                                                         APPLICANT: Cardineau, Guy A.
APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman. Steven J.
APPLICANT: Narva, Kenneth B.
TILE OF INVENTION: Plant-Optimized Genes Enc FILE REFERENCE: MA-114XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/178,252
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-23
SOFTWARE: PALENT UNOS: 27
SOFTWARE: PALENT UNOS: 27
LENGHALE: 3558
                                 ; Sequence 22, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
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Best Local Similarity 66.5%;
Matches 2458; Conservative C
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                  US-09-826-660-22
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                                                                                                                           GCTTTATTTGTAGATTCTCAATATAGATTACAAGCGGATACAACATTGGCATGATT
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TTGGATATTGATATTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGTATTTC
                  TIGGATATTGATGTTGGATGCACAGACTTGCATGAGAATCTAGGCGTGTGGGGTGGTATTC
                                                             AAGATTAAGACGCAGGAAGGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAAA
                                                                                                                                            CGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAGAAGCTGTGGAT
                                                                                                                                                                                                             CATGCGGCAGATAACTTGTTCATCGAATTCGAGAGGCTTATCTGTGAATTATCTGTT
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TTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAACGTTATTATGAGCGCCAAG 661

1673 GAGTTAGATACGCTGCTTCTCAAACTATGGTTCTTAGAGTTACTGTTGGAGGATCTACTA 1732 1736 CTTTTGATCAAGGATTCCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTACTAT 1795 1733 CTTTGATCAAGGATTCCCATCTATGTCTGCTAACGAGTCTCTTACTTCTCAATCTT 1792 1796 TTAGATTTGCAAATTCCTGTAGGTATTAGTGCATCTGGCAGTCTAACTGCTGGAATAA 1855 1796 TTAGATTTGCAAATTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAA 1855 1793 TCAGATTCGCTGAGGTATAGTGCATCGGCTCTGGATCTTAGATAGCAGCTGGAATCT 1852 1856 GTATAAGTAATAATGCAGGTAGAAACGTTTCATTCATAAAATTGAAATTCCAA 1915	191 197 197 203	AGTATCCAATTTAGTGGCGTGTTATCGGATGAATTCTGGTTAGATGAAAAGAGAAT 209	2156 CAAACTTCACATCAATAAGCAACCAGACTTCATATCTACTAATGAGCAATT 2215	233		2456 ATGCGAAACATGGATGTTCCAGGTACCGAGTCCGTATGGCGGCTTTCAGTTG 2515	TCCTGCAGAGATGGAGAAAATGTGCGCATCATTCCCATCATTTTT	2696 TCAAGATTAAGACGCAGGAAGTCATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGA 2755
8 6 8 6 8 6	8 6 8 6	6 6 6 6	8 6 8 6	8 8 8	g & g	8 6 8 6	8 6 8 6	8685
	782 842 842 902	902 CICCARCIGGATICGCITCTACTAACAACAACAACAACCACTCCATCTTCTCTGCTA 961 QY 956 TAGAGACTGCGCTATCCGAAGCCCGCATCTACATTTCTAGAACAACTTACAATTT 1015	TTCAATCTCGGCCAATAGGAGGCGGATTAAATACCTCAAGGCTGGGGTCTACCCAATACTT	1196 CAGGAGICCTICIAGITCACTICIAGAGAIGIGTACAGAACTGAGTCTTTCG 120 1196 CAGGAGICCTICIAIGGGGAAITIACCTICAAACCTATICAIGGGGCCTACTGTTAGAI 125			1435 AACICITIAGAACICCAGIGIACICITIGGACICATAGAACICAGATAGAACTAACACCA 1496 TIAGITCAGATAGCATAACACAAATACCATTGGAAAATCATTCAACTTAATTCAGGA 1493 TCTCTTCTGATTCTATCACTCAGATTCCACTTGTGAAGTCTTTCAACTTGAACTCTGAA 1556 CCTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGAATATAATCCGAACTAACGTAATG 1553 CTTCTGTAGTCAGTGGCCCAGGATTTACAGGAGGGAATATAATCCGAACTAACGTTAATG 1553 CTTCTGTAGTTGTTTCTGAACCAGAATTTACAGGAGGAACAACAACAACAACAACAACAACAACAACAA	1616 1613 1676

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Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
INVENTION: SYTHETIC DNA SEQUENCE HAVING ENHANCED
INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATES SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. US20030046726A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
                                                                                                        NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS: 94
ADDRESSEE: SYNGENta Biotechnology,
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
Crossland, Lyle D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3624 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.7%;
Matches 2310; Conservative C
                                                                                                                                                                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                        TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-988-462-6
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                                                                                                                                                                                   2801 TTCATGCTGCAGACAAACGCGTTCATAGCATTCGGGAAGCTTACCTTCCTGAACTTAGCG
                                                                                                                                                                                                                                                                                                                                           TCTCCTTGTATGATGCGAGGAATGTCATCAAGAATGGTGACTTCAACAATGGCCTATCCT
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             AACGTGAAAAACTACAATTGGAAACAAAACGAGTATATACAGAGGCAAAAAGAAGCTGTGG
                                             2681 AGAGAGAAGTTGGAATGGGAACAAACATTGTGTACAAGAAGGCGAAGGAAAGCGTTG
                                                                                      ATGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTGGCATGA
                                                                                                                        2741 ACGCTCTGTTTGTGAACTCTCAGTATGATAGGCTCCAAGCTGATACCAACATAGCTATGA
                                                                                                                                                             TTCATGCGCCAGATAAACTTGTTCATCGAAATTCGAGAGGCTTATCTGTCAGAATTATCTG
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139 ATCAATCCACTTGTTAGCGCATCAACAGTCCAAACGGGTATTAACATAGCTGGTAGAATA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGCGTGCTGGCCTTCGCCGGCCAGCTGCTTCTACAGCTTCTGGTG 180
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                                                                                                                                                                                                                                                                                                                    79 ATGGATCTATCACCAGATGCTCGTATTGAGGATTCTTTGTGTATAGCCGAGGGGAATAAT
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                              Length 3624;
                                                                                                                                                                                                                                                                                   15;
                                                                                                            LOCATION: 1..3621
OTHER INFORMATION: /product= "Full-length, maize
                                                                                                                                                                                                                                          Score 1495.6; DB 10; Lengt
Pred. No. 0;
0; Mismatches 1299; Indels
                                    = "Synthetic DNA
                                                                                                                                                   optmized crylB"
/note= "Disclosed in Figure 6.
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
TOPOLOGY: linear
MOLECULE TYPE: other nucleic
DESCRIPTION: /desc = "Sy
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Exercial, Michael G. Desai, Nalini M. Lewis, Kelly S. Kramer, Vance C. Warren, Gregory W. Evola, Stephen V.

Sequence 6, Application US/09988462 Publication No. US20030046726A1 GENERAL INFORMATION: APPLICANT: Koziel, Michael G

RESULT 6 US-09-988-462-6

	Qy 1399 AGTCATAGGTTATCTCACATAGGGCTCATTTCACAATCTAGGGTGCATGTACATATAT 1458	QY 1459 TCTTGGACGCACCGTAGTGCAGATCGTACAAATACCATTAGTTCAGATAGCATAACATAACATA 1518 DD 1381 AGCTGGACCACCGACCGACCGACCAACCATCGGCCCCAACCGCATCACCCCAG 1410	1519	OY 1579 TTTACAGGAGGATATAATCCGAACTAACGTTAATGGTAGTACTAAGTATGGGTCTT 1638	OY 1639 AATTTAATAATACATCATTACAGGGTATGGCGTGAGAGTTCGTTATGCTGCTTCTCAA 1698	Qy 1699 ACAATGGTCCTGAGGGTAACTGTCGAGGAGTACTATTTGATCAAGGATTCCCTAGT 1758 Db 1621 GACTTCGACTTCTTCGTGAGCCGCGGCGCCACCACGTGAAACTTCCGCTTCCTGCGC 1680	Qy 1759 ACTATG AGTGCAAATGAGTCTTTGACATCTCAATCATTTGGAGATTTCCT 1815 Db 1681 ACCATGAACAGCGGCGACGAGCTGAAGTACGGCAACTTCGTGCGCCGCGCCTTCACCACC 1740	Qy 1816 GTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATAAGTATAATGCAGGT 1875 DD 1741 CCCTTCACCTTCACCCAGAACATCCAGGACATCCACCAGCACAGCATCCAGGGCCTGAGCGGC 1800	OY 1876 AGACAAACGTTTCACTTTGATAAATTGAATTCATTCAATTACTGCAACCTTCGAAGCA 1935 DD 1801 AACGGCGAGGTGTACATCGACAAGATCGAACCCCGGTGACCGCCACCTTCGAGGCC 1860	Qy 1936 GAATACGATTTAGAAAGGCGCAAGAGCGGTGAATGCTCTGTTTACTAATACGAATCCA 1995 Db	Qy 1996 AGAAGATTGAAAACAGATGACAGATTATCATATTGATCAAGTATCCAATTTAGTGGCG 2055	Qy 2056 TGTTTATCGGATGAATTCTGCTTAGAAAAGAGAGAAATTACTTGAGAAAGTGAAATAT 2115	QY 2116 GCGADACGACTCAGTGATGADAGADACTTACTCCAAGATCCAACTTCACATCATCAT 2175 DD 2041 GCCADGCCTGAGCGCAACCTGCTGCTGCAGGACCCCAACTTCACCAGCATCAAC 2100	QY 2176 AAGCAACCAGACTTCATATTATTACTAATGAGCAATTGGAATTTCACATCTATCCATGAACAA 2235 DD 2101 AAGCAGCCCGACTTCATCAGCAACGAGGAACTTCACCAGGATTCACCAGGAGCAG 2160	Qy 2236 TCTGAACATGGTGGGGAAGTGAGAACATTACAATCCAGGAAGAAATGACGTATT 2295 Db 2161 AGCGAGCACGGTGGGGCAGCAAACATCACCATCCAGGAGGCAACGACGACGTTC 2220	Oy 2296 AAAGAGAATTACGTCACCTACCGGGGACTTTTAATGAGTGTTATCCGACGTATTTATAT 2355	Oy 2356 CAAAAATAGGAGGTCGGAATTAAAAGCTTATACTCGCTACCAATTAAGGGGTATATT 2415 Db 2281 CAGAAGATCGGCGAGAGGGGAGGCCTACACCCGCTACCAGCTGCGCGCGGTACATC 2340	Qy 2416 GAAGATAGCAAGATTTAGAGATATTTGATTCGTTATAATGCGAAACATGAAACATTG 2475
259 GGTGAATTATGGCCCGGGGGAGATCAGTGGGAAATTTTCCTAGAACATGTCGAACAA 318 	319 CITATADATCAACAAATAACAGAAAATGCTAGGAATACGGCACTTGCTCGATTACAAGGT 378			499 AATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCATTATTAATGGTATATGCT 558	559 CAAGCTGCAAATTTACACCTATTATTATTATTGGAGATGCCTCTTTTTGGTAGATTT 618	619 GGGCTTACATCGGGAAATTCAACGTTATTATGAGCGCCAAGTGGAACAAACGAGAAT 678 	679 TATTCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAATAGCTTGAGAGGGACAAAT 738		CTAGTGGCACTATTCCCAAGCTATGACCTCGCACTATCCAATAAAACGACTGCTCAG 858	918 840	978	1038 960	1098	1158	1218	1278	ACTITIGAAAGAGGTACTGCTAACTATAGTCAACCCTATGAGTCACCTGGGCTTCAATA 1338	AAAGATTCAGAAACTGAATTACCACCAGAAACAACAGACGACCAAATTATGAATCATAT 1398

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267 GGAAAGGAACCGGGCAATTACTACATTACGAGGSTTAGCAGATAGCTATGAAATTTATAT 326
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                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09826660

Sequence 5, Application US/09826660

Sequence 5, Application US/09826660

GENERAL INCRMATION:

APPLICANT: Cardineau, Guy A.

APPLICANT: Stelman, Steven J.

APPLICANT: Stelman, Steven J.

TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

FILE REFERENCE: MA-114XC2D1

CURRENT PILING DATE: 1001-04-05

CURRENT PILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-23

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1998-03-02

PRIOR SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 27
                                                        3481 GTGAACTACCCCCCCCCGCGCCGCCTACGTGACCAAGGAGCTGGAGTACTTCCCCGAG
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Pred. No. 0;
0; Mismatches 1061; Indels 108; Gaps
                                                                                                                                                                                      GAATTACTCCTTATGGAGGAATAG 3687
                                                                                                                                                                                                                    3601 GAGCTGCTGATGATGAGAGAGTAG 3624
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Best Local Similarity 65.7%;
Matches 2243; Conservative (
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GAGGACAGCCAGGACCTGGAGATCTACCTGATCCGCTACAACGCCAAGCACGAGACCCTG
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                                                                                                                                                                                                                                                                                                                                                  Score 1408.4; DB 11;
Pred. No. 0;
0; Mismatches 1061; I.
PRIOR FILING DATE: 1994-03-17
PRIOR APPLICATION NUMBER: US 07/865,168
PRIOR FILING DATE: 1992-04-09
PRIOR APPLICATION NUMBER: US 07/451,261
PRIOR FILING DATE: 1989-12-14
PRIOR FILING DATE: 1989-12-17
PRIOR PELICATION NUMBER: US 371,955
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                               ; ORGANISM: Bacillus thuringiensis US-09-837-961-7
                                                                                                                                                                               SOFTWARE: Patentin version 3.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                Query Match 38.2%;
Best Local Similarity 65.7%;
Matches 2243; Conservative (
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APPLICANT: Sick, August
APPLICANT: Sick, August
APPLICANT: Sick, August
TITLE OF INVENTION: No. US20040058860Alel Bacillus thuringlensis Isolate Active Again
TITLE OF INVENTION: and Genes Encoding No. US20040058860Alel Lepidopteran-Active Tox
FILE REFERENCE: MA-43CDF2D3
CURRENT APPLICATION NUMBER: US/09/837,961
CURRENT PILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/521,344
PRIOR FILING DATE: 1097-09-19
PRIOR FILING DATE: 1097-09-19
PRIOR FILING DATE: 1997-09-19
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                                                    2751 GAATATTGCCATGATTCATGCGGCAGATAAAACGTGTTCATAGAATTCGGGAAGCGGTATCT
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Publication No. US20040058860A1
GENERAL INFORMATION:
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Oy 345 TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404	525 AAACCAAGAAGTTCCATTATTAATGGTATATGCTCAAGCTGCAAATTTACACCTATTATTATTATTATTATTATTATTATT	OY 585 ATTGAGATGCCTCTTTTTGGTGAATTTGGGCTTACATCGCAGGAAATTCAACG 644	QY 645 TTATTATGAGCGCCAAGTGGAACAAACGAGATTATTCCGACTATTGCGTAGAATGGTA 704 Db 567 TCATTATAATAATAAATCTTATTCATAGATATACGAAAACATTGTTTGGACACATA 626	OY 705 TAATACAGGTCTAAATAGCTTGAGAGGGACAAATGCCGCAAGTTGGGTGCGTTATAATCA 764	Qy 765 ATTCCGTAGAGATCTAAGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA 824	Qy 825 CACTGGCACTTATCCAATAAATAGGGGGGGCTGCTTAACAAGGGAAGTTTATACAGAGGC 884	QY 885 AATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTGGTATAATAATGCACCTTC 944 Db 807 AGTAATTGAGATTCTCCAGTTTCTGCTAATATACCTAA 845	QY 945 GTTTTCCGCTATAGAGACTGCGGTTATCCGAAGCCGCATCTAGATTTTCTAGAACA 1004	QY 1005 ACTTACAATTTTTAGCACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGGGG 1064 Db 903TTCTTTGTAACTGCAGAGACTGTTAGAAGTCAAACTGTGTGGGGAGG 953	Qy 1065 GGGGCACACAATTCAATCTCGGCCAATAGGAGGGGGGATTAAATACCTCAACGCATGGGTC 1124 Db 954 ACACTTAGTTAGTTCACGAAATACGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGT 1013	Qy 1125 TACCAATACTTCTATTAATCCTGTAAGATTATCATTCTTCTCTCGAGACGTATATTGGAC 1184 Db 1014 CTTCAATCCTGGTGGCGCCATTTGGATTGCAGATGAGGATCCACGTCCTTTTTATCGGAC 1073	Qy 1185 TGAATCATATGCAGGAGTGCTTCTATGGGAATTTACCTTGAACCTATTCATGGTGTCCC 1244 Db 1074 ATTATCAGATCCTGTTTTGTCCGAGGAGGATTTGGGAATCCTCATTATGTACT 1127	Qy 1245 TACTGTTAGATTTAGGAACCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTA 1304 Db 1128 GGGGCTTAGGGGAGTAGCATTTCAACAACTGGTACGAACCACCCGAACATTAGAAA 1187	OY 1305 TAGTCAACCCTATGAGTCACCTGGGCTTCAATTAAAGATTCAGAAACTGAATTACCACC 1364	OY 1365 AGAACAACAACAAATTATGAATCATATAGTCATAGGCTTATCTCACATAGGGCT 1424 Db 1247 GGAATGATTATAGTCATTAAATCATGTACATTGTACGATGCCAGTGAGTTT 1306 OY 1425 CATITCACAATCTAGGGTGCATGTACCATATTGGACGCACGTAGTGTT 1340
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Qy 3279 TGTAACGATCCATGAAATCGAGAACAJ Db 3111 CGTAACCATTCATGAGATCGAGAACAQ Qy 3339 AGAGGAGTCTATCCAACGGATCACG Db 3171 AGAGGAGTCTATCCAACAACACACGC Qy 3399 AGCAGTATGTAATTCCCGTAJ Db 3231 ATACGGGGGTGCGTACCATCCCGTAJ	Oy 3453 TACAGCATCTGTTAATTACAAACGA(Db 3291 TTCTGTACCAGCTGATTATGCGTCAG	Qy 3513 AGATAATCATTGTGAATATGACAGAG Db 3351 AGACAATCCTTGTGAATCTAACAGAG	OY 3573 TATGACAAAGAATTAGAATACTTCCC	OY 3633 AACGGAAGGGAAGTTTATTGTAGACGGGGGAATTACTCCTTATGGAGGAA 	RESULT 9 US-10-825-751-7	sequence 7, Application US/10825/51 sequence 7, Application No. US20040194165A1 general information: Applicant: Payne, Jewel	## AFPLICANI SICK, AUGUST 0. TITLE OF INVENTION: Novel Bacillus the TITLE OF INVENTION: Pests, and Genes FILE REFERENCE: MA-43CDF2D4	NT FILING DATE: 2004-04 APPLICATION NUMBER: US FILING DATE: 2001-04-15	APPLICATION NUMBER: US FILING DATE: 2000-03-05 APPLICATION NUMBER: US FILING DATE: 1997-09-15	APPLICATION NUMBER: US FILING DATE: 1994-12-14 APPLICATION NUMBER: US FILING DATE: 1994-03-17	APPLICATION NUMBER: US FILING DATE: 1992-04-09 APPLICATION NUMBER: US FILING DATE: 1989-12-14	; PRIOR APPLICATION NUMBER: US 371,955 ; PRIOR FILING DATE: 1989-06-27 ; NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: Patentin version 3.2	; SEQ 1D NO 7 ; TYPE: DNA ; OKGANISM: Bacillus thuringiensis	38.2%; Scc milarity 65.7%; Pre Conservative 0:	QY 285 TCAGTGGGAATTTTCCTAGAACAGTGGGAACAACTTATAATCAACAAATAACA Db 207 TGATTGGAGCTTATTCTTTTACAGATTGAACAATTGATTG

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CAACTTACAATTTTTAGCACTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTGG 1062
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ATTTAGAAGAGAATTAACACTAACTGTATTAGATATCGTTTCCTATTCCGAACTATGA
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Sequence 25, Application US/09873873

Sequence 25, Application US/09873873

Sequence 25, Application US/09873873

Sequence 25, Application US/0965A1

GENERAL INFORMATION:

APPLICANT: Gilmer, Amy Jelen

TITLE OF INVENTION: Polymucleotide Compositions Encoding Broad-Spectrum S-Endotoxins

FILE REFERENCE: MECO. 210--2

CURRENT FILING DATE: 1099-02-19

FRIOR APPLICATION NUMBER: US 08/253,341

PRIOR FILING DATE: 1999-02-19

PRIOR FILING DATE: 1999-09-03

PRIOR PILING DATE: 1999-09-03

PRIOR FILING DATE: 1996-11-20

SPRIOR FILING DATE: 1996-11-20

SPRIOR FILING DATE: 1996-11-20

SPRIOR FILING DATE: 1996-11-30

TRIPE: DATE: 1996-11-30

SEQ ID NOS: 35

LENGTH: 3534

TYPE: DNA

TYPE: DNA

ORGANISM: Artificial Sequence
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                                                                   Gaps
                                                                  66
                                                 Length 3534;
                                                                  Indels
                                               Score 1402; DB 10;
Pred. No. 0;
0; Mismatches 1070;
; OTHER INFORMATION: Hybrid Delta-Endotoxin; NAME/KEY: CDS
LOCATION: (1) .. (3531)
US-09-916-956A-25
                                              Query Match
Best Local Similarity 65.7%;
Matches 2243; Conservative
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1172 GGGGGGGGGGGGGGGTTTTGATCOAGGTTTAAAACAAATGGGTGCAAATGGGTGCCTTT 1612 1623 TGGGGGGGGGGGGGTTTTTAACTGGGGTTTAAAACAGGTTTAAAACAGGTTTAAAACAGGTTTAAAACAGGTTTAAAAACAGGTTTAAAAACAGGTTTAAAAAACAGTTTAAAAAAAA
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Pred. No. 0;
0; Mismatches 1070; Indels
              PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 09/253,341
PRIOR FILING DATE: 1999-02-19
PRIOR FILING DATE: 1999-02-19
PRIOR PILING DATE: 1997-09-03
PRIOR APPLICATION NUMBER: US 08/754,490
PRIOR FILING DATE: 1996-11-20
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
LENGTH: 3534
                                                                                                                                                                                                                          OTHER INFORMATION: Hybrid Delta-Endotoxin
                                                                                                                                                                                                                                                                                                                    38.0%;
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Best Local Similarity 65.7
Matches 2243; Conservative
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US-10-365-645-25
                                                                                                                                                                                               ORGANISM: Artificial
                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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US-10-356-645-25
US-10-366-645-25
Feduence 25. Application US/10365645
Fublication No. US20030182682A1
GENERAL INFORMATION:
APPLICANT: MAIVAR. Thomas
ITILE OF INVENTION: Amy Jelen
TITLE OF INVENTION: Delta-Endotoxins (Amended)
FILE REPERENCE: 11792.01.0 DVUS02 (MECO:210-3)
CURRENT APPLICATION NUMBER: US/10/365,645
FRICK RING DATE: 2003-02-12
FRICK APPLICATION NUMBER: US 09/873,873
GGCAAAAGAAGCTGTGGATGCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGA
                                                                 2709 GGCAAAAGAATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATCAATACAAGGGA
                                                                                                        TACAAACATTGGCATGATTCATGCGGCAGATAAACTTGTTCATCGAATTCGAGAGGGCTTA
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1993 GANTGAMAGCAGAMATTGTCCGAGAMGTCAAACATGCAAACATCAAACAACAACAACAACAACAACAACAACAACA
1063 GGGTHATRATRATICATIONACIONANGANGGATATANANGGATATANANGGATANANGGATATANANGGATATANANGGATATANANGGATATANANGGATATANANGGATANANG

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584 512 644 572 704 632 764 692

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TCGTTTTCCGCTATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAA 1002
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TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404
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                     273 CGCTAGGAACCAAGCATTTCTAGATTAGAAGGACTAAGCAATCTTTATCAAATTTACGC
                                                                   ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTA
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| Publication No. US20040093637A1
| GENERAL INFORMATION:
| APPLICANT: Malvar, Thomas
| APPLICANT: Gilmer, Amy Jelen
| TITLE OF INVENTION: Polynuclectide Compositions Encoding Broad Spectrum
| TITLE OF INVENTION: Polynuclectide Compositions Encoding Broad Spectrum
| TITLE OF INVENTION: Polynuclectide Compositions Encoding Broad Spectrum
| TITLE OF INVENTION: Ablance 11792.0215.DVG902 MECO:215--2
| CURRENT APPLICATION NUMBER: US/10/672,163
| FRIOR APPLICATION NUMBER: US 09/261,040
| PRIOR APPLICATION NUMBER: US 09/261,040
| PRIOR FILING DATE: 1999-03-02
| PRIOR FILING DATE: 1996-01-20
| PRIOR FILING DATE: 1996-01-20
| PRIOR FILING DATE: 1996-01-20
| PRIOR FILING DATE: 1996-11-20
| SOFTWARE: Patentin Version 3.2
| SEQ ID NO 2: 30
| SEQ ID NO 2: 30
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Pred. No. 0;
0; Mismatches 1070; Indels
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ORGANISM: Artificial sequence
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38.0%;
Best Local Similarity 65.7%;
Matches 2243; Conservative (
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; LOCATION: (1)..(3531)
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943 TCGTTTTCCGCTATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAA 1002
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633 CAATACGGGATTAGAGCGTGTATGGGGGACCGGATTCTAGAGATTGGATAAGATATCA 692
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                                                                                                                   ATTTAGAAGAATTAACACTAACTGTATTAGATATCGTTTCTCTATTTCCGAACTATGA
                                                                                                                                                                        CACTCGCACTTATCCAATAAATACGAGTGCTCAGTTAACAAGGGAAGTTTATACAGAGGC
                                                                      ATTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA
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                                                                                         RESULT 15
US-10-739-482-25
i Sequence 25, Application US/10739482
i Sequence 25, Application US/10739482
i Publication No. US20040132975A1
i REDERAL INFORMATION:
i APPLICANT: Mohan, Komarlingham S.
APPLICANT: Sivasupramaniam, Sakuntala
ITILE OF INVENTION: Delta-Endotoxina
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ITILE OF INVENTION: Delta-Endotoxina
ITILE OF INVENTION: UNUMBER: US 6,242,241
PRIOR APPLICATION NUMBER: US 6,242,241
PRIOR PILING DATE: 1999-02-19
PRIOR PILING DATE: 1999-02-19
PRIOR PILING DATE: 1996-11-20
INUMBER OF SEQ ID NOS: 35
IEMARE: PatentIn version 3.2
IEMARTH: SAM
ITVEE: DNM
ORGANISM: Artificial sequence
FRATURE:
COMPANISM: Artificial sequence
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Pred. No. 0;
0; Mismatches 1070; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 65.7%;
Matches 2243; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-10-739-482-25
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us-10-614-524-1.rnpb

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us-10-614-524-1.rst

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November 21, 2004, 08:54:06; Search time 10040 Seconds (without alignments) 13381.802 Million cell updates/sec
                                                                                                                                                                                                  US-10-614-524-1
3687
1 ttgacttcaaataggaaaaa......tactccttatggaggaatag 3687
                                                                                                                                                                                                                                                                                                                                                                                          65645750
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                               32822875 segs, 18219865908 residues
                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                  Title:
Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

9b est1: 9b htc: 9b est3: 9b est4: 9b est6: 9b 9s81: 9b 9s82: EST: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			do			SOUTHER	
Result No.	ult No.	Score	Query Match	Query Match Length DB	DB	ΩI	Description
	-4	61	1.7	880	8	AZ669474	AZ669474 ENTIY88TR
	7	59	1.6	908	œ	. AZ548467	
υ	٣	57.4	1.6	843	œ	AZ551618	AZ551618 ENTDV54TR
	4	55.8	1.5	748	σ	BX137558	BX137558 Danio rer
	Ŋ	55.2	1.5	931	œ	BH160272	BH160272 ENTQV49TR
υ	9	52.8	1.4	1101	σ	CNS0039G	AL063921 Drosophil
U	7	52.4	1.4	877	œ	AZ531291	AZS31291 ENTBQ34TR
U	æ	52	1.4	849	œ	AZ546009	AZS46009 ENTFW53TF
	σ	51.8	1.4	886	ß	BX422107	BX422107 BX422107
	10	51.8	1.4	1101	σ	CNSOOEVL	AL069706 Drosophil
	11	51.2	1.4		œ	AZ549980	AZ549980 ENTDD94TF
บ	12	51	1.4	1101	σ	CNSOOEMH	AL069378 Drosophil
υ	13	51	1.4	1337	σ	AG280055	AG280055 Mus muscu
	14	50.6	1.4	912	ω	AZ551092	AZ551092 ENTFJ22TF
	15	50.2	1.4	467	4	BM163521	BM163521 EST566044
υ	16	49.8	1.4	1253	σ	AG289789	AG289789 Mus muscu
U	17	48.8	1.3	1064	4	BM416119	BM416119 OP21205 M
	18	48.6	1.3	890	80	AZ530768	AZ530768 ENTBH54TF
	19	48.4	1.3	543	4	BI397189	BI397189 kt58a11.y
υ	20	48.4	1.3	905	œ	AZ550256	AZ550256 ENTEV58TR
	21	48.4	1.3	1101	0	CNS0106X	AL098595 Drosophil
U	22	47.6	1.3	828	œ	AZ669217	AZ669217 ENTFV38TR
	23	47.6	1.3	906	œ	AZ529180	AZ529180 ENTCE59TR
υ	24	47.6	1.3	939	œ	AZ540454	AZ540454 ENTDF66TF

	BM164708 EST567231	AL060767 Drosophil	BJ403374 BJ403374	BH149983 ENTQD93TF	BJ363051 BJ363051	BJ363776 BJ363776	BJ366397 BJ366397	AG444032 Mus muscu		AG347197 Mus muscu	BU498625 PfESToab9	BI670654 PfESToaa0	BI814240 PFESToaal	BU496406 PfESToac0	BH149893 ENTPK44TR		BJ386441 BJ386441	BJ383101 BJ383101	AZ671853 ENTLQ71TF	BJ444006 BJ444006
CNS0100X	BM164708	CNS005TE	BJ403374	BH149983	BJ363051	BJ363776	BJ366397	AG444032	CNS00Z6Z	AG347197	BU498625	BI670654	BI814240	BU496406	BH149893	BJ384484	BJ386441	BJ383101	AZ671853	BJ444006
σ	4	σ	4	œ	4	4	4	σ	σ	6	'n	4	4	Ŋ	œ	4	4	4	80	4
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1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3
47.6	47.4	47.4	47	47	46.8	46.8	46.8	46.8	46.8	46.8	46.6	46.6	46.6	46.6	46.6	46.4	46.4	46.4	46.4	46.2
25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

AZ669474 BNT1Y89TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence. AZ669474 AZ669474. GI:11806620			/dlone libe "Entemocha histolytica Sheared DNA" /olone libe "Entemocha histolytica Sheared DNA" /note="Vector: pHOS1; Site_1: BRt I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entemocha histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome
RESULT 1 AZ669474 LOCUS DEFINITION ACCESSION VERSION	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	

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3093
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S Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica HM1: IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9343
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1: IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTEK3OTR Entamoeba histolytica Sheared DNA linear GSS 14-NOV-2000 genomic, genomic survey sequence.
AZ548467
AZ548467.1 GI:11172102
                                                                                                                                                                                                                                                                                                                                                                                        TCCACCACTACCAGCTGGTTATATGACAAAAGAATTAGAATACTTCCCAGAAACCGATAA 3611
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                                                                                                                                                                                                                                                                                                    372 TGATGAAGATGATGATGATGATGAAGACGAATATGAATTAGAAGATGATGGATTATT
 and
                                                                                                           3252 GIACAAAGAGGGATATGGAGGGTTGTGTAACGATCCATGAAATCGAGAACAATACAGA
                                                                                                                                     Gaps
Sequencing: A Practical Approach, eds. M. Vaudin
Barell, Oxford University Press, 1999)."
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                                                     Length 880;
                                                    Score 61; DB 8; Length 880
Pred. No. 0.00037;
0; Mismatches 230; Indels
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High quality sequence start: 17
High quality sequence stop: 828.
Location/Qualifiers
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Seg primer: M13-Reverse
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ilarity 46.4%;
Conservative (
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Entamoeba histolytica
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                                                    Query Match
Best Local Similarity
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/clone_libe_Entramoba histolytica Sheared DNA"
/clone_libe_Entramoba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
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Best Local Similarity 44.2%;
Matches 337; Conservative
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Submitted (127-374-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: hunguery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 95C15. 95C15 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:

Keygene. Further details:

http://www.sanger.ac.uk/Projects/D_rerio/.
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Danio rerio genomic clone DKBY-95C15, genomic survey sequence.
BX137558
                          AGAAGGTCGCATTATCACTGCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGG 3092
                                                                                                              TGATTTTAATAATGGATTAGCATGCTGGAATGTAAAAGGGCCATGTAGATGTACAACAGAG 3152
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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                                                                   3273 GGGTTGTGTAACGATCCATGAAATCGAGA---ACAATACAGACGAACTAAAATTTAAAAA
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/note="vector pindigoBAC-536"
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/clone="DKEY-95C15"
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/note="Vector: pHOS1; Site 1: Bst 1; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of B. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome
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DNA library
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                                                                                                                                                                                                                                     Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 843)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
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USA
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                                                                                              B43 bp DNA ENTDV54TR Entamoeba histolytica Sheared Genomic, genomic survey sequence. AZ551618 GENOMIC 511176919 GSS.
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 9208
Fax: 301 838 3543
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/strain="HM1:IMSS"
/db xref="taxon:5759"
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High quality sequence start: 39
High quality sequence stop: 838.
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/note="Vector: pHOS1; Site_1: Bet_1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
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SNTQV49TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                           CTCCAAGATTCAGAAGAAGATTCAGAAGAAGAATTCAGAAGAATTCAGAAGAA
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 931)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1: IMSS sheared DNA library (2001)
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       DB 9; Length 748;
1.5%; Score 55.8; DB 9; Length 7.45.8%; Pred. No. 0.0077; d. 45.8%; Pred. No. 0.0077;
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 9263
Fax: 301 838 3543
Email: bjloftus@etigr.org
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/strain="HM1:IMSS"
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High quality sequence stop: 677.
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                    Best Local Similarity 45.8 Matches 192, Conservative
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila and managester BAC library was prepared by Kazucoyo Goegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoxI digestion of Drosophila DNA provided by the BDGP From the BDGP's and BSGP in and EST libraries. A more detailed description of the library
              G.G., and Diamond, L.S. (1993) Entamoba histolytica: a method for isolate identification. Exp. Parasitol. 7:450.) The DNA was mechanically sheared to give a fight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, Ho. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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1.5%; Score 55.2; DB 8; Length 9
Best Local Similarity 47.4%; Pred. No. 0.012;
Matches 165; Conservative 0; Mismatches 183; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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al Similarity 15.7%; Pred. No. 0.05;
99; Conservative 264; Mismatches 269; Indels
                                                                       /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="taxon:7227"
/clone="laxORRN10"
/clone="lab=RRPC1-98"
/note="end : TET3"
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/db_xref="taxon:5759"
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/clone lib="Entamoeba histolytica Sheared DNA"
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Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1991) Entamoeba histolytica: a
method for isolate identification. Bxp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
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                                                                          from Entamoeba histolytica
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                                                                                                                                                                       Contract: Brendan J Loftus
Contract: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 9208
Fax: 301 838 3543
Email: bloftus@tigr.org
Clones are derived from the Entamoeba
DNA library
Seq primer: M13-Reverse
Class: shotgun
1 (bases 1 to 877)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence start: 22
High quality sequence stop: 829.
Location/Qualifiers
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 886)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-langth cDNA libraries and normalization

Unpublished (201)

On May 13, 2003 this sequence version replaced gi:30651307.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Brail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

lst strand cDNA was primed with a Not!-011go(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned was not normalized. Library division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Tunitoche Nor Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division of Every Labrary division o
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                                  314 İGATGAİGATGAAGAAGAAĞAAGAAĞAĞATĞATGAİĞAATTTĞAAİTAĞAAĞATGA 255
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BX422107 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA clone CS0DH007YD10 3-PRIME, mRNA sequence.
                                                                                           3108 ATTAGCATGCTGGAATGTAAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGT
                                                                                                                                                                                                                                                                      374 AGAİGAİGAAGATĞAİGAİĞAİĞAİĞAİGAIGAİĞAİĞAİĞAİĞAİGAAĞAİ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                division of Invitrogen.
This sequence belongs to sequence cluster 3628.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODH007DB05NP1&c=3628.r.
Location/Qualifiers
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/ Ab Xref="taxon:559"
/ Clone_lib="Entamoeba histolytica Sheared DNA"
/ Ance="Vector: PHOS1); Site_1: Bsf I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: C.G., and Diamond, L.S. (1993) Entamoeba histolytica: method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tiel library construction is described in detail in Smith, H.O. and Venter, J.C. (Maxing small insert libraries for Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                          ISM Entramocha histolytica
Eukaryota; Entamochidae; Entamocha.

Eukaryota; Entamochidae; Entamocha.

Loftue, B., Van Aken.S. and Fraser, C.

Loftue, B., Van Aken.S. and Fraser, C.

Determination of clone end sequences from Entamocha histolytica
HM:IMSS Sheared DNA library
Unpublished (2000)

Contact: Brendan J Loftus
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9543

Email: bjloftus@tigr.org
Clones are derived from the Entamocha histolytica HM:IMSS sheared
DNA library
Seq primer: M13-Forward
Class is shotgun
High quality sequence start: 26
High quality sequence start: 36
Llocation/Qualifiers
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Sheared DNA Entamoeba histolytica
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1.4%; Score 52; DB 8; Length 849;
Best Local Similarity 43.3%; Pred. No. 0.075;
Matches 296; Conservative 0; Mismatches 385; Indels
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/mol_type="genomic DNA"
/strain="HM1:IMSS"
                                                                                                                     genomic, genomic survey sequence.
                                                                     ENTFW53TF Entamoeba histolytica
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 ENYR cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuctoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the loggenic strain y2; co bw may by, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                             1851 AATAAGTATAAGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTGAATTCAT 1910
                                                                                                                                                                                                        1911 TCCAATTACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAA 1970
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                                                                                                                                                     206 TGGAATATTGTCCAAAAATWATWCAAAGGAAWGGAAWAAGAATKGAACAACAKATWAAAA
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                       Length 886;
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
|Clone="BACR2953"
                                                                        Best Local Similarity 38.6%; Pred. No. 0.085;
Matches 118; Conservative 34; Mismatches 154;
                                                     DB 5;
Library was not normalized."
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Drosophila melanogaster
                                                     Score 51.8;
Pred. No. 0.
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AL069706
AL069706.1 GI:4949849
                                                   1.4%;
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BNTDD94TF Entamoeba histolytica Sheared DNA linear GSS 14-NOV-2000 GNTDD94TF Entamoeba histolytica Sheared DNA Entamoeba histolytica AZ549980 AZ549980.1 GI:11175122 AZ54980.1 GI:41175122
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Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 900)
Loffus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
                                                                                                                                                                                                                                                                TCCAATTACTGCAACCTTCGAAGCAGAATACGATTTAGAAAGGGCGCAAGAGGCGGTGAA
                                                                                                                                                                                                                                                                                            WWAATWIWWAAAWAAAWITATWAATWAAAAWAWWWAITITIWWWWWIWATIWITWAW
                                                                                                                                                                                                                                                                                                                                                                                               710 ААМААТИАТАМАТААМТТАААМААТАААМААМААТИАММАТАТАТИМАТАТАМТТ
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                   DB 9;
                                                                                                            0.09;
                                                                                     Score 51.8;
Pred. No. 0.
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/note="end : T7"
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                                                                                1.4%;
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                                                                                                                                                   Fax: 301 838 3543
Email: bjloftus@tigr.org
Conse are derived from the Entamoeba histolytica HM1:IMSS sheared
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BACR29M06 of RPCI-98 library from Drosophila melanogaster (fruit AL068378
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
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48.0%; Pred. No. 0.12;
tive 0; Mismatches 158; Indels ;
                                                                                                                     organism="Entamoeba histolytica"
                              DNA library
Seq primer: M13-Forward
Class: shorgun
High quality sequence start: 20
High quality sequence stop: 890.
Location/Qualifiers
                                                                                                                                     mol_type="genomic_DNA"
|strain="HM1:IMSS"
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Best Local Similarity
Matches 146; Conserv
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AL Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :

- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information melanogaster genome using these BACs. For further information melanogaster pack is prepared by Kazutoyo Geoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of NY. The library us prepared by Kazutoyo Geoegawa and Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, BCSKI digestion of Drosophila DNA provided by the BDGP from the BOGP is and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualiflers

Source Genetic Center can be Location/Qualiflers
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Mus musculus molossinus DNA, clone:MSMg01-051D13.T7, genomic survey
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GSS.
Mus musculus molossinus
Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1.4%; Score 51; DB 9; Length 110;
Best Local Similarity 32.0%; Pred. No. 0.14;
Matches 102; Conservative 69; Mismatches 148; Indels
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/organism="Drosophila melanogaster"
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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/clone lib="RPCI-98"
/note="end : T7"
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632 TDGGGKKRDKRTDGGRWGT 614
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/db xrefe="taxon:5759"
/db xrefe="taxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site=1: BSE 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of B. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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                            Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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                                                                                           Unpublished (2000)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
721. 301 838 9543
Email: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI
DNA librari
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 17
High quality sequence store
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
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                                                                                                                                                                                       and Chemical Research (RIKEN) Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriegger.riken.jb, UKL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba 35-0074 Japan
Koyadai, Tsukuba 35-0074 Japan
Phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                     Submitted (17-NOV-2003) Magahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3311
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                                                                                                             Hattori,M., Toyda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
                              Kojima, T. and Sakaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 51; DB 9; Length 1337; 49.4%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus molossinus"
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Hattori,M., Toyoda,A., Noguchi,H., K
BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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/db_xref="taxon:57486"
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Entamoeba histolytica
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/dev stage="Masxual blood stages"
//dev stage="Masxual blood stages"
//lab_host="E. coil XL-1 Blue"
//clon=llab="Myss"
//note="Wector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB-GByJ mice infected with Py17XL parasites, and leukcoytes removed by passage over microcrystalline cellulose collumns. Total RNA was month solated using the guandidinium isothiocyanate method, and First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dcTP. After second strand synthesis, uneven stamply dcTP. After second strand synthesis, uneven adaptors ligated to the blunt ends The sample was cleaved with KNoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA mas precipitated to the blunt ends The sample was cleaved Size-fractionated cDNA was precipitated to HybrizAP arms directionally using EcoR-XhoI cleaved arms. exclsed from the HybriZAP vector (pAD-GAL4) was exclsed from the HybriZAP vector and plasmid DNA was read and plasmid DNA was precipitated to the high and separated and ligated to After packaging, the phagemid vector (pAD-GAL4) was
                                                                                     GAAGAAACGTATACAGATGTACGAAGATAATCATTGTGAATATGACAGAGGGTATGTG
                                                                                                                                                                                           3547 AATTATCCACCACTACCAGCTGGTTATATGACAAAGAATTAGAATACTTCCCAGAAACC 3606
BM163521
ESTS66044 PyBS Plasmodium yoelii yoelii cDNA clone PYCLG23 5' end,
                                                                                                                                                                                                                                     Email: caritonerigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 467)
Carlton,J.M., Daly.T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Praser.C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9112 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism="Plasmodium yoelii yoelii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sub_species="yoelii"
/db_xref="taxon:73239"
/clone="PYCLG23"
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/strain="17XL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRVA sequence.
BM163521
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FEATURES

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                                                                                               249 TAGAAAATGAAAATATGAAAAAGGCGATGAAATAGAAGATAAAAATATGAAATAGAAG 308
                                                                                                                                                                                                                           309 ATGADADATATGADATAGADADADADATATGADATAGADGATADADADATAG 368
                                                                                                                                                                                                                                                                                                  3350 ATCCAACGGATACAGGAACGTGTAATGATTATACTGCACAAGGTACAGGAGTATGTA
                                              Gaps
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              Length 467;
Query Match
1.4%; Score 50.2; DB 4; Length 4
Best Local Similarity 48.7%; Pred. No. 0.19;
Matches 136; Conservative 0; Mismatches 143; Indele
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Compugen Ltd.
GenCore version (c) 1993 - 2004
         Copyright
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OM protein - protein search, using sw model

November 21, 2004, 13:33:31 ; Search time 119 Seconds (without alignments) 3701.845 Million cell updates/sec Run on:

6479 1 LTSNRKNENBIINALSIPAV......IGETEGKFIVDSVELLLMEE 1228 US-10-614-524-2 score: Title: Perfect (

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 seqs, 358729299 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:* Database :

geneseqp1980s:* geneseqp2000s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003bs:* geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	uo.
	6479	100.0	1228	4	AAB84628	Aab84628	Amino aci
7	6462	99.7	1228	4	AAU02039		B. thurin
m	5926.5	91.5	1227	~	AAW44321	Aaw44321	Bacillus
4	5926.5	91.5	1227	4	AAB19950	Aab19950	Bacillus
S	5912.5	91.3	1227	4	AAU02046	Aau02046	B. thurin
9	5740	88.6	1228	N	AAR50955	Aar50955	Bacillus
7	5436.5	83.9	1227	~	AAY31990	Aay31990	Chimeric
80	5237.5	80.8	1229	~	AAR54074	Aar54074	CryETS. 2
Đ	5237.5	80.8	1229	~	AAW35259	Aaw35259	Bacillus
10	5237.5	80.8	1229	~	AAW17699	Aaw17699	CryETS. 3
11	5237.5	80.8	1229	~	AAW87633	Aaw87633	CryETS pr
12	5237.5	80.8	1229	N	AAY30923	Aay30923	B. thurin
13	5237.5	80.8	1229	æ	ADK98479	Adk98479	B thuring
14	5233.5	80.8	_	œ	ADK98484	Adk98484	B thuring
15	5233.5	80.8	1230	œ	ADK98489	Adk98489	B thuring
16	5233.5	80.8	_	œ	ADK98481	Adk98481	B thuring
17	5233.5	80.8	1230	00	ADK98491	Adk98491	B thuring
18	5233.5	80.8	1230	œ	ADK98487	Adk98487	B thuring
19	5189.5	80.1	1209	4	AAU02094	Aau02094	Bacillus
20	5183.5	80.0	-	4	AAU00421	Aau00421	B. thurin
21	5169.5	79.8	_	4	AAU00420	Aau00420	B. thurin
22	5108	78.8	1186	N	AAY16796	Aay16796	Amino aci
23	4791	73.9	1208	4	AAU02093	Aau02093	Bacillus
24	4303.5	66.4	1217	4	AAU02092	Aau02092	Bacillus
25	3977.5	61.4	1174	ď	AAR89494	Aar89494	B.t. toxi

Aaw09043 Bacillus	Aar25825 Novel tox	Aar08257 B.thuring	Aaw46737 Amino aci	Aaw47035 Bacillus	Aar63231 Crystal p	Aar54073 CryET4. 2	Aaw35258 Bacillus	_	Aaw87632 CryET4 pr	Aay30922 B. thurin		Aay17783 EG12111 c	Aay82431 Bacillus	Aae26471 Bacillus	Abg93849 B. thurin	Abw02350 B. thurin	Aaw61335 A mutated	Aay17788 B. thurin	Aay82396 Bacillus
AAW09043	AAR25825	AAR08257	AAW46737	AAW47035	AAR63231	AAR54073	AAW35258	AAW17700	AAW87632	AAY30922	AAW61345	AAY17783	AAY82431	AAB26471	ABG93849	ABW02350	AAW61335	AAY17788	AAY82396
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1174	1174	1174	1176	1176	1170	1167	1167	1167	1167	1167	1189	1189	1189	1189	1189	1189	1189	1189	1189
61.4	61.3	61.3	58.5	58.5	55.2	54.9	54.9	54.9	54.9	54.9	54.1	54.1	54.1	54.1	54.1	54.1	54.0	54.0	54.0
3977.5	3974.5	3969.5	3791	3791	3579	3556	3556	3556	3556	3556	3502.5	3502.5	3502.5	3502.5	3502.5	3502.5	3500.5	3500.5	3500.5
56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

The present sequence represents CrylBf, an insecticidal protein derived from Bacillus thuringiensis. The specification also describes CrylJd and CryPRa. The Cry proteins have activity against lepidopteran and coleopteran insect pests. CrylBf, CrylJd and Cry9Fa polynucleotides and polypeptides are useful for obtaining a plant with resistance to insects. Cry polynucleotides are useful for producing transgenic plants which are resistant to insects. CrylBf; insecticidal protein; CrylJd; Cry9Fa; lepidoptera; coleoptera; insect pest; transgenic plant. Novel insecticidal proteins CrylJd, Cry9Fa and CrylBf, derived from Bacillus thuringiensis, useful for controlling insects in plants. Van Rie J; Arnaut G, Boets A, Damme N, Mathieu E, Vanneste S, Amino acid sequence of a CrylBf insecticidal protein. AAB84628 standard; protein; 1228 AA Claim 11; Page 37-41; 65pp; English. (AVET) AVENTIS CROPSCIENCE NV. 19-DEC-2000; 2000WO-EP013184. 99US-0173387P. (first entry) Bacillus thuringiensis. WPI; 2001-425619/45. N-PSDB; AAH28240. WO200147952-A2. 28-DEC-1999; 05-SEP-2001 05-JUL-2001 AAB84628; AAB84628

Sequence 1228 AA;

Gaps ö DB 4; Length 1228; Indels ö 100.0%; Score 6479; 100.0%; Pred. No. 0; iive 0; Mismatches Query Match
Best Local Similarity 100.
Matches 1228; Conservative

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RVTAYKEGYGEGCVTIHEJENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNSRN 1140
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                             1081 RYTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNSRN
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Bacillus thuringiensis. WO200119859-A2.

22-MAR-2001.

13-SEP-2000; 2000WO-US025361.

99US-0153995P 15-SEP-1999;

(MONS) MONSANTO CO

Rupar MJ Gilmer AJ, Donovan WP, chu c, Baum JA,

2001-281518/29. N-PSDB; AAS02482 Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the insect resistance of plant.

Claim 5; Page 139-141; 173pp; English.

The sequence represents a B. thuringiensis Lepidopteran-active delta-endotoxin, crystal protein CryBT64. The Lepidopteran-active B. thuringiensis delta-endotoxin polypeptides may be used as compositions that are applied to plant crops to protect them from insect damage. The polymorleotides may be used in the production of transgenic plants that express the insecticidal polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicotyledonous plants may be protected in this way, for example corn, tobacco, kapok, flax, potato, barley, turf grass, pagture grass, berry, truit, lagime, vegetable, ornamental plant, shrub, cactus and/or tree fruit, lagime, vegetable, ornamental plant, shrub, cactus and/or tree cell. A wide range of insects (e.g gypsy moth, looper, tobacco budworm, cotton leaf perforator and spruce budworm) may be affected by application of the insecticidal polypeptides (full details given in specification)

Sequence 1228 AA;

Gaps ö 99.7%; Score 6462; DB 4; Length 1228; 99.6%; Pred. No. 0; :ive 3; Mismatches 2; Indels 0 Conservative Query Match Best Local Similarity Matches 1223; Conserv

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RVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCNSRN
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                                                                                                                                                                                                                             Bacillus thuringiensis 158C2c toxin.
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Matches 1129; Conservative
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RVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQCTAACNSRN
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The present sequence is that of the C-terminal region of novel delta-endotoxin 1582Cc of Bacillus thuringiensis (B.t.) isolate PS158C2 (NRRL B-18872). The amino acid sequence is predicted from a partial gene sequence for 1582Cc (See AAA82222) obtained from a PS15BC2 gene library. The invention provides novel B.t. delta-endotoxins 1582Ca-d (see AAB1994.7-50), which are active against leplodpteran pests. Expression of the delta-endotoxins in transformed plants confers resistance to these insect pests, while transformed microorganisms can be applied to sites where they will proliferate and be ingested by the pest
                                                                                                                                                                                                                                                                                                                                                                                           New genes isolated from Bacillus thuringiensis which encode toxins against lepidopteran insects and which can be used to transform various hosts to express the B.t. toxin and confer insect resistance.
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91.8%; Pred. No. 0;
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transgenic plant; insect
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Matches 1129, Conservative
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N-PSDB; AAA89221.
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                                                                                              NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA
                                          LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP
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toxin; lepidoptera; crystal protein; resistance; crop protection; biological control.
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The sequence represents B. thuringiensis Lepidopteran-active delta-endotoxin, crystal protein CryBT54. The Lepidopteran-active B. thuringiensis delta-endotoxin polypeptides may be used as compositions that are applied to plant crops to protect them from insect damage. The cypress the insect damage. The polynucleotides may be used in the production of transgenic plants that express the insectical polypeptides and consequently have improved insect resistance compared to non-transformed plants. Monocotyledonous or dicotyledonous plants may be protected in this way, for example corn, what, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato, ctobacco, kapek, flax, potato, barley, turf grass, pasture grass, berry, fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm, cotton leaf perforator and spruce budworm) may be affected by application of the insecticidal polypeptides (full details given in specification).

Cotton leaf perforator and spruce budworm) may be affected by application cotton leaf perforator and spruce activated and spruce assigned explicitly in the specification, cryETS number assigned to any Seq.1D number, the indexer has matched the spare sequence cotton least assigned to any Seq.1D number, the indexer has matched the spare sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides and the polynucleotides that encode them, useful for increasing the insect resistance of plant.
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ive 36; Mismatches
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                    AAU02046 standard; protein; 1227
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Matches 1127; Conservative
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        SLRGTNAASWVRYNOFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG
                                                             LARLOGIGDSFRAYQOSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP
                          LLMVYAQAANLHLLLLRDASLFGSEFGLTSQBIQRYXERQVEQTRDYSDYCVEWYNTGLN
                                    V--NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT
                                                                                                             IQSRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVR
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The CryIB toxin gene (disclosed in EP-408403) has been found to be toxic to the European corn borer (Ostrinca nubilalis). The use of CryIB insecticidal crystal protein for protecting crops against O.nubilalis is claimed. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method to control or combat Ostrinia - utilises Bacillus thuringiensis cry IB gene/protein for crop prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis; (strain entomocidus HD 110)
                                                                                                                                                                                                                                                                                           Bacillus thuringiensis CryIB insecticidal protoxin
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                                                                                                                                                                                                                                                                                                                                      Insecticidal crystal protein, ICP, cryIB, Ost
European corn borer, Lepidoptera, Pyralidae,
88.6%; Score 5740; Di
89.0%; Pred. No. 0;
ive 36; Mismatches
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                                                                                                                             standard; protein; 1228
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(first entry)
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Best Local Similarity 89.0
Matches 1097; Conservative
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Insecticide, HyPLIB; crystal protein; delta-endotoxin; toxin; crylB; crylA(b); maize; transgenic plant; European corn borer; Ostrinia nubilalis; entomocide; crop protection; biological control.

Chimeric CrylB insecticide HyFLIB,

Location/Qualifiers

thuringiensis.

Bacillus t Synthetic.

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               296 VNMASMYWYNNNAPSFSAIBAAAIRSPHLLDFLEQLTIPSASSRWSNTRHWTYWRGHTIQ
                                                                                                            FGPIRVTVNGPLTQRYRIGFRYASTVDFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFV
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                                                SRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFN
                                                              356 SRPIGGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFN
                                                                                               FRIPONTFERGTANYSOPYESPGLOLKDSETELPPETTERPNYESYSHRLSHIGLISOSR
                                                                                                                                                VHVPVYSWTHRSADRINTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGS
                                                                                                                                                                                               VLSMGLNFNNTSLORYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFR
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AAY31990 standard; protein; 1227

(first entry)

05-JAN-2000

AAY31990,

RESULT 7
AAY31990
ID AAY3
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AC AAY3
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DT 05-J

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This sequence represents a chimeric insecticidal protein, termed hyFLIB, that is composed of a crylB core N-terminal toxin portion of 845 amino acids and a crylA(b) C-terminal protoxin portion of 382 amino acids. The crylB and crylA(b) portions of the synthetic gene (see AAZ20086) encoding HyFLIB were derived from Bacillus thuringiensis with codon usage altered to increase expression in plants, particularly maize. When the chimeric insecticidal protein gene is expressed in transgenic maize from both PEPC and pith promoters, insecticidal activity is observed against Buropean corn borer (Ostrinia mubilalis). Recombinant microbial strains transformed with the hyFLIB gene can be used in endotmocidal formulations for the biological control of Lepidopteran pests
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                                                                                                                                                                                                                                                                                                                                                                                                                                    protein comprising cryIB and cryIA(b)
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84.3%; Pred. No. 0;
ive 63; Mismatches
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES
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                                                                                                                                                                                /note= "crylA(b)"
                                                                                                                                    1. .845
/note= "crylB"
846. .1227
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Matches 1040; Conservative
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                 cryETS;
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                                                                                                                                       Isolated cryET4
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                       insecticidal
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                                             US5322687-A
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                       SRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTVRFN
                             VHVPVYSWTHRSADRINTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGS
                                               FRNPONTFERGTANYSOPYESPGLOLKDSETELPPETTERPNYESYSHRLSHIGLISQSR
                                                                              VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFR
                                                                                                                     FAEFPVGISASGSQT-AGISISNNAGRQTFHFDKIEFIPITATFEABYDLERAGBAVNAL
                                                                                                                             FINTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDP
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<sup>15</sup>; Lepidoptera; lepidopteran insect; insecticidal; toxin;
crystal protein; ICP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA
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79.9%;
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Best Local Similarity 79.9
Matches 983; Conservative
                                         Bacillus thuringiensis.
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Ostrinia nubilalis; Pseudoplusia includens; Plutella xylostella;
Spodoptera exigua; Spodoptera frugiperda; Trichoplusia ni.
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                                                                                                                                                                                               CryBT5, which, optionally in association with B. thuringiensis EG7283, can be used against lepidopteran peste. CryBT5 is especially useful for controlling Lymantria dispar, Ostrinia mubilalis, Beeudoplusia includens, Plutella xylostella, Spodoptera exigua, Spodoptera frugiperda and
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                                                                                          - useful
                                                                                                                                                                                crystal
                                                                                                                                                                                                                                                                                                                                                Length 1229;
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                                                                                                                                                                                Bacillus thuringiensis EG7283
                                                                                          protein
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; Pred. No. 0;
94; Mismatches
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This sequence represents the cryETS protein of Bacillus thuringiensis

(B.t.) isolate EG5847. B.t. produces inclusions during sporulation which
include insecticidal crystal proteins (TCP). ICP toxins are active in
the circled elisecticidal crystal proteins (TCP). ICP toxins are active in
the midgut cells, resulting in cessation of feeding, and eventually
the CryI proteins produced by B.t. are active against lepidopteran
consects. This protein, and the CryET4 protein (see AMM17700) belong to
the CryI family of ICPs. The DNA encoding this sequence can be used to
consects which are useful as insecticides against a wide range
consecuency of lepidopteran peets, and can be applied to crops, soil and seeds. This
protein, or especially its toxic N terminal region, can be expressed in
consecuency provide protection against lepidopteran peets. The gene
concoding this sequence, or its fragments, can also be used to isolate
concoding this sequence. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                       Query Match 80.8%; Score 5237.5; DB 2; Length 1229; Best Local Similarity 79.9%; Pred. No. 0; Matches 983; Conservative 94; Mismatches 149; Indels 5;
                             Claim 1; Fig 2; 50pp; English.
                                                                                                                                                                                                                                                              Sequence 1229 AA;
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for control of lepidopteran pests.
DPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFN
                                                                                                               VESPIGRCGEPURCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWV
                                                                                                                                                                   ECYPTYLYOKIGESELKAYTRYOLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLS
                                                                                                                                                                                                                                                            VDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIIT
                                                                                                                                                                                                                                                                                                                                                                                          1079 YILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAAACN
                                                                                                                                                                                                                                                                                                                                                                                                                                               SRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCBYDRGYNYYPPLPAGYMTKELB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CryET5; cryET4; Bacillus thuringiensis; insecticidal crystal
ICP; toxin; CryI protein; lepidopteran insect; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFPETDITVWIEIGETEGKFIVDSVELLLMEE 1229
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(first entry)
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Gonzalez JM,

30-DEC-1993; 29-JUL-1993;

US5616319-A 01-APR-1997

25-MAR-2003 07-JUL-1997

CryET5; CryETS.

AAW17699;

'n,

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The present sequence represents a CryETS protein. The protein is isolated from a new strain of Bacillus thuringiensis (B.t.), strain EG5847 (NRRL B -21110). EG5847 contains two new crystal toxin genes (cryET4 and cryET5) that produce proteins active against Lepidoptera. CryET4 is more active than CryIA(a) against Helicoverpa zea, resistant-strains of Plutella active than CryIB against S. frugiperda, while CryET5 is more active than CryIB against S. frugiperda and Trichoplusia ni (and both are active against additional insect species)
                                                                                                                                                                                                                                                                               V--NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT
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Pred. No. 0;
94; Mismatches
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Best Local Similarity 79.9
Matches 983; Conservative
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RCYPNYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTDSLWPLS
                                                                                                   VPKI KTQEGYARLGNLEPI EEKPLIGBALSRVKQAEKKWRDKREKLQLETKRVYTEAKEA
                                                                                                                                                                                       VDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNABIFEELEGRIIT
                                                                                                                                                                                                    VDALFVDSQYDQLQADTNIGMIHAADKLVHRIREAYLSELPVIPGVNAEIFEELEGHIIT
                                                                                                                                                                                                                                                      1079 YILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEBEEVYPTDTGTCNDYTAHQGTAACN
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                                      ECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLS
                                                                                      VESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWV
                                                                                                                                      VFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEA
                                                                                                                                                                                                                                       AISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRG
                                                                                                                                                                                                                                                                                       YILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCN
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                                                                                                                                                                                                                                                                                                                                                                                         YPPETDKVWIRIGETEGKFIVDSVELLLMEE 1228
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93US-00176865.
95US-00474038.
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JB; AAV83927.
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30-DEC-1993;
07-JUN-1995;
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61 NIAGRILGVLGVPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQLIRQQVTENTRNTA 120
       insecticidal proteins with activity against a broad spectrum of insects of the order Lepidoptera. This sequence represents the cryET5 protein described in the method of the invention
                                                                                                                                                                                  LARLOGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP
                                                                                                                                                                                                                        NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDOWEIFLEHVEQLINQOITENARNTA
                                                                                                                                                                                                                                                                          241 NLRGTNAESWLRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIGRTN
                                                                                                      1 LISNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI
                                                                                                                  241 SLRGTNAASWVRYNOFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATG
                                                                                                                                                                                                                                                                                                    301 V -- NMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT
                                                                                                                                                                                                                                                                                                                APSGFASTNWFNNNAPERSAIEAAIFRPPHLLDFPEQLIIXSASSRWSSTQHMVYWVGHR
                                                                                                                                                                                                                                                                                                                                          359 IQSRPIGGGLNTSTHGST-NTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTV
                                                                                                                                                                                                                                                                                                                                                      RFNFRNPQNTFERGTANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLIS
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                                                                    2; Length 1229;
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                                                                80.8%; Score 5237.5; DB 2;
79.9%; Pred. No. 0;
iive 94; Mismatches 149;
                                                                          Local Similarity 79.9%;
tes 983; Conservative
                                              Sequence 1229 AA;
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                                                 VDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIIT
                                                                                        AISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRG
VESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel transformed plants containing Bacillus thuringlensis strain EG5847 insecticidal crystal protein genes cryET4 cryET5. cryET4 and cryET5 are novel toxin genes which produce
                                                                                                                                                                                                                                                                                                                                                                                   cryET5; insecticidal; Lepidoptera; transformed plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            start codon
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                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .1229
/note= "partial protein sequence. No ATG
given"
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                                                                                                                                                                                                                                               Donovan WP;
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93US-00176865.
95US-00474038.
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30-DEC-1993;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide sequence optimized for expression of an insecticidal protein in a plant, useful in the control of Lepidoptera insect pests, and for producing transgenic plants with the ability to resist insect
VDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFBELEGRIIT
                AISLYDARNVVKNGDFNNGLACMNVKGHVDVQQSHHRSYLVIPEWEAEVSQAVRVCPGRG
                                                                           SRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPVPAGYVTKELE
                                                                                                                 YILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAVCN
                                                                                                                                                                          SRNAGYEDAYEVDTTASVNYKPTYEETTYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELE
                                                                                                                                                                                                                                                                                                                                                                                                                               thuringiensis crylBb partial protein sequence SeqID2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           insecticidal protein; plant; pesticide; gene therapy; lepidopteran insect pest; transgenic plant; insect infestation resistance; monocot; dicot; crylBb.
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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N-PSDB; ADK98478.
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                                                       LTSNRKNENEI INALSI PTVSNPSTQMNLSPDARI EDSLCVAEVNNI DPPVSASTVQTGI
                                                                               NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA
                                                                                                                    LARLOGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP
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                                       LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI
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                     Gaps
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  Length 1229;
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  DB 8;
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; Score 5237.5;
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94; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide sequence optimized for expression of an insecticidal protein in a plant, useful in the control of Lepidoptera insect pests, and for producing transgenic plants with the ability to resist insect
 AISLYDARNVVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRG
             YILRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQCTAVCN
                                                                              SRNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELE
                                                                                           expression cassette protein SegID7,
                                                                                                                                                                                                                                                                     insecticidal protein; plant; pesticide; gene therapy;
lepidopteran insect pest; transgenic plant;
insect infestation resistance; monocot; dicot; crylBb.
                                                                                                                     YFPETDKVWIRIGETEGKFIVDSVELLLMEE 1228
                                                                                                                                 Claim 7; SEQ ID NO 7; 138pp; English.
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(BOGD/) BOGDANOVA N N.
(ROMA/) ROMANO C P.
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                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis. Synthetic.
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                                                                                                                                                                                       ADK98484 standard;
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N-PSDB; ADK98482.
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                                                                               LMVYAQAANLHILILIRDASILFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGINS
                                                                                                                                                                                     LRGTNAASWVRYNOFRDLTLGVLDLVALFBSYDTRTYPINTSAQLTREVYTDAIGATGV
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Conservative 94; Mismatches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an insecticidal
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MSLYDARNVVKNGDFNNGLTCWNVKGHVDVQQSHHRSDLVI PEWEAEVSQAVRVCPGRGY
                  ILRVTAYKEGYGEGCVTIHEIENNTDELKFROCEEEVYPTDTGTCNDYTAHQGTAVCNS
                                                                    1081 İLRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTAACNS
                                                           RNAGYEDAYEVDTTASVNYKPTYEBETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEY
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                                                                                                                                                                                                                                                       icidal protein; plant; pesticide; gene therapy;
pteran insect pest; transgenic plant;
infestation resistance; monocot; dicot; crylBb
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80.8%; Score 5233.5;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 982; Conservative 94; Mismatches
                                                                                                              PPETDKVWIRIGETEGKFIVDSVELLLMEE
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                                                                                                                                                                         ADK98489 standard; protein; 1230
                                                                                                                                                                                                                                    thuringiensis crylBb-related
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N-PSDB; ADK98488.
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insect infest
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TSNRKNENBIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEVNNIDPFVSASTVQTGIN
                                                       IAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVBOLINQOITENARNTAL
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No.
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Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 59, Appl Sequence 59, Appl Sequence 59, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli		thuringiensis Delta-Endotoxin	; Length 1228; 2; Indels 0; Gaps 0;	SLCIAEGNNINPLVSASTVQTGI 60 	EIFLEHVEQLINQQITENARNTA 120 	YIALELDFLNAMPLFAIRNGEVP 180 	ERQVEGTRDYSDYCVEWYNTGLN 240 	TYPINTSAQLTREVYTDAIGATG 300 	IPSTSSRWSATRHMTYWRGHTIQ 360
1 US-08-032-364-2 1 US-08-100-709-2 1 US-08-176-865-2 1 US-08-474-038-2 2 US-08-811-340-2 2 US-08-811-340-2 2 US-08-811-340-2 3 US-09-314-091-59 9 4 US-09-317-635-59 9 4 US-09-317-636-2 9 2 US-08-980-071-2 9 3 US-09-314-093-2 9 3 US-09-314-093-2 9 3 US-09-314-093-2 9 3 US-09-317-636-2 9 3 US-09-317-636-2 9 3 US-09-317-636-2 9 3 US-09-317-636-2 9 3 US-09-317-636-2 9 3 US-09-317-636-2 9 4 US-09-317-636-2	ALIGNMENTS	ion US/09661322A les A. h-Rei william P. Amy J. lark J	.7%; Score 6462; DB 4 .6%; Pred. No. 0; e 3; Mismatches	LTSNRKNENBIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI -	NIAGRILGVLGVFFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 	LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLPAIRNQEVP 	LLMVYAQAANLHLLLLRDASLFGSFGLTSQBIQRYYERQVEQTRDYSDYCVEWYNTGLN 	SLRGTNAASWVRYNQFRRDLTLGVLDLVALPPSYDTRTYPINTSAQLTREVYTDAIGATV 	VRMASMRWYRNRAESFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIO
3579 55.2 1170 3556 54.9 1167 3556 54.9 1167 3556 54.9 1167 3556 54.9 1167 3502.5 54.1 1189 3502.5 54.1 1189 3502.5 54.1 1189 3502.5 54.1 1189 3500.5 54.0 1189 3500.5 54.0 1189 3500.5 54.0 1189 3500.5 54.0 1189 3500.5 54.0 1189 3500.5 54.0 1189		1 661-322A-38 ence 38, Applicat mt No. 659329; RAL INFORMATION: LICANT: Baum, Jam LICANT: Chu, Chi LICANT: Glimer, LICANT: Baum, Jam LICANT: Rupar, M LICANT: Rupar, M LICANT: Rupar, M LE OF INVENTION: ER REFERENCE: MECO RENT FILING DATE: BER TO SEQ ID NOS RENT FILING DATE: BER OF SEQ ID NOS RENT FILING DATE: RENT FILING DATE: BER OF SEQ ID NOS RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT FILING DATE: RENT RENT RENT RENT RENT RENT RENT RENT	Match Match Socal Similarity 9	1 LTSNRKNENEIINA : 1 MTSNRKNENEIINA	61 NIAGRILGVLGVPF 	121 LARLOGIGDSFRAY 121 LARLOGIGDSFRAY	181 LLMVYAQAANLHLI 181 LLMVYAQAANLHLI	241 SLRGTNAASWVRYN 241 SLRGTNAASWVRYN	301 VNMASMNWYNNNAE 301 VNMASMNWYNNNAE
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Sequence 8, Application US/08448170

Sequence 8, Application US/08448170

Sequence 8, Application US/08448170

GENERAL INFORMATION:

APPLICANT: Cummings, David A.

APPLICANT: Cummings, David A.

APPLICANT: Cummings, David A.

APPLICANT: Cummings, David A.

APPLICANT: Stelman, Steve

TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
                                                                                                                             FAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEABYDLERAQEAVNALF 660
                                                                                                                                                                                          TNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPN 720
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          VHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIRTNVNGS
                                                                                       VLSMGLNFNNTSLQRYRVRVRYRAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFR
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::
TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran ITILE OF INVENTION: Encoding Lepidopteran-Active Toxins NUMBER OF SEQUENCES: 10
CORRESPONDENCES: ADDRESS: ADDRESSSER: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
CITY Gainesville STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1227,
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MEDIUM TYPE: Flopyy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,170
FILING DATE: U-JUNE-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: U-JUNE-1993
CLASSIFICATION 1424
PRIOR APPLICATION 1424
PRIOR APPLICATION WINBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION NUMBER: 31.794
ATTORNEY AGENT INFORMATION:
NAMME: Saliwanchik, David R.
REGISTRATION NUMBER: M/S 102D.CI
TELEPHONE: (904) 375-8800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 amino acide
TWENT: amino acide
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Matches 1129; Conservative
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MOLECULE TYPE: peptide
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STRANDEDNESS: Bil
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61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDPWEIFLEHVEQLIRQQVTENTRDTA 120
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION DATA:

PILING DATE:

APPLICATION NUMBER: US/08/961,803

FILING APPLICATION B00

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/069,902

FILING DATE: 01-JUNE-1993

CLASSIFICATION: 800

PRIOR APPLICATION: 800

PRIOR APPLICATION NUMBER: US 07/759,247

FILING DATE: 13-SEPT-1991

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/448,170

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/448,170

FILING DATE: 23-MAY-1995

CLASSIFICATION: 800

CLASSIFICATION: 800
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91.8%; Pred. No. 0;
ative 36; Mismatches
                      3: Jay M. Sanders
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SANGER, Jay M.
REGISTATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: M/S 102DCD1
TELECOMMUNICATION INFORMATION:
                  ADDRESSEE: Jay M. Sanders
STREET: 4241 N.W. 41st Street, Sui
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (352) 375-8100
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Matches 1129; Conservative
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Patent No. 6150589
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
NUMBER OF SEQUENCES: 10
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                                      419 FNFRNPONTFERGTANYSOPYESPGLOLKDSETELPPETTERPNYESYSHRLSHIGLISO
361 LESRTIRGSLSTSTHGNTNTSINPVTLQFTSRDVYRTESFAGINI---LLTTPVNGVPWAR
                                                                 538 GSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQS
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US-08-961-803-9
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120

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                                                                                                                      Indels
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                                                                                                                      62;
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                                                                                                Query Match
91.3%; Score 5912.5;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1127; Conservative 36; Mismatches
       CURRENT APPLICATION NUMBER: US/09/661,322A CURRENT FILING DATE: 2000-09-13 NUMBER OF SEQ ID NOS: 63 SEQ ID NO 63 LENGTHR: 1227
                                                            TYPE: PRT ORGANISM: Bacillus thuringiensis
                                                             ; TYPE: PRT
; ORGANISM: Bac:
US-09-661-322A-63
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Patent No. 6593293
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APPLICANT: Baum, James A. APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupar, Mark J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compose FILE REFERENCE: MECO201
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89.4%; Pred. No. 0;
ive 34; Mismatches
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.4°
Matches 1079; Conservative
                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                  ; MOLECULE TY1
US-07-951-715A-7
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                      958 DALFVDSQYDRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA
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                                                                                                                                   DALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITA
                                                                                                                                                                                                                                             ISLYDARNVVKNGDFNNGLACMNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGY
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APPLICANT: Deesi, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Lewis, Kelly S.
APPLICANT: Lewis, Kelly S.
APPLICANT: Warren, Gregory W.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Blis J.
APPLICANT: Rochstell, Stewn L.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowen, Cindy G.
APPLICANT: Bowen, Cindy G.
APPLICANT: Bowen, Cindy G.
APPLICANT: Bowen, Cindy G.
APPLICANT: Bowen, Strik M.
APPLICANT: Bowen, Strik M.
APPLICANT: Bunder, Brik M.
APPLICANT: Bunder, Brik M.
APPLICANT: Bunder, Strik M.
APPLICANT: Buttie, Janet L.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHA
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE
STREET: 7 SKYline Drive
COURTES OND SECOND STRIKE
CITY: Hawthorne
STATE: New York
COUNTRY: USA
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE: CASEP-1992
CLASSIFICATION: 800
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REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-07-951-715A-7
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61 GELWPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSC 865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526 RQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA
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                                                                                                                                                                                                                                                                                                  Length 1207;
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                              ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: GCC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEFHONE: (919) 541-858
TELEFHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TUPOLOGY: linear
                                                                                                                                                                                                                                                                                          87.4%; Score 5659.5;
89.4%; Pred. No. 0;
ive 34; Mismatches
                  04-OCT-1991
INFORMATION:
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Best Local Similarity 89.4%
Matches 1079; Conservative
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                  FILING DATE:
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                                                           VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH
                                                                                                                        1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGGGYILRVTAYKGGYGEGCVTIHEIENNTDE
                                  LSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL
                                                                                                                                                                       VDVQQSHHRSVLVI PEWEAEVSQAVRVCPGRGYI LRVTAYKEGYGEGCVTIHEIENNTDE
                                                                                                                                                                                                                                        LKFKNCEBEBUYPIDIGICNDYIAHQGIA----VCNSRNAGYEDAYEVDITASVNYKPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
Desai, Nalini M.
APPLICANT:
Desai, Nalini M.
APPLICANT:
Lewis, Kally S.
APPLICANT:
Warren, Gregory W.
APPLICANT:
Barlen, Stephen V.
APPLICANT:
Crossland, Lyle D.
APPLICANT:
Meriln, Blis J.
APPLICANT:
Launis, Karen L.
APPLICANT:
Dewenn, Cindy G.
APPLICANT:
Dewenn, Cindy G.
APPLICANT:
Dewenn, Cindy G.
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Dewenn, Cindy G.
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Dewenn, Cindy G.
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APPLICANT:
Dewenn, Cindy G.
APPLICANT:
Dewenn, Cindy G.
APPLICANT:
Dewenn, Cindy G.
APPLICANT:
APPLICANT:
Bree, Gary M.
APPLICANT:
APPLICANT:
Suttle, Janet L.
TITLE OF INVENTION:
SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION:
SYNTHETIC DNA SECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SECTIFFACES.
94
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ZIP: 10591-9005

ZIP: 10591-9005

COMPUTER 1850ABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION 1995
FILING DATE: 02-UNN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 94 CONTROLLED ACTIVITY IN MALZE CORRESPONDENCE ADDRESS: 4 ADDRESSE: No. 5859336artis Corporation STREET: Patent & Trademark Dept., 520 White Plains STREET: Rd., POB 2005
CITY: Tarrycown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
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US-08-459-448A-7
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89.4%; Pred. No. 0;
ive 34; Mismatches
                APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
                                                                                                                                                                                                                                                 1207 amino acids
                                                                                                                                                                                             TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              Matches 1079; Conservative
                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                   linear
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US-08-459-595A-7
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EEETYTDVRRDNHCEYDRGYVNYPPLPACYMTKELEYFPETDKVWIEIGETBGKFIVDSV
                                                  RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA
                                                                                                                 LSRVKRABKKWRDKREKLQLETKRVYTEAKBAVDALFVDSOYNRLOADTNIGMIHAADKL
                                                                                                                                                                               VHRIREAYLSELSVI PGVNAEI FEELEGRIITAI SLYDARNVKNGDFNNGLACWNVKGH
                                                                                                                                                                                                                                              VDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE
                                                                                                                                                                                                                                                                            1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKEGYGEGCVTIHEIENNTDE
                                                                                                                                                                                                                                                                                                              LKPKNCEREEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY
                                                                                                                                                                                                                                                                                                                                            LKPKNREBEBVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVNYKPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pace, Gary M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarryown
STATE: New York
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ZIP: 10591-9005
ZIP: 10591-9005
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN RN-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF BACKERY APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
APPLICATION NUMBER: US/08/459,595A
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Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Liyle D.
Wright, Martha S.
Merlin, Blils J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08459595A
Patent No. 6018104
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| ELLLMEE 1207
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US-08-459-595A-7
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APPLICANT:
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87 GELWPRGRDOWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRD 146
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                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy
REGISTATION NUMBER: 38,241
REFERENCE DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMNUNICATION INFORMATION:
TELEFAX: (919)541-8687
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERICSTICS:
LENGTH: 1207 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.4%; Score 5659.5;
89.4%; Pred. No. 0;
Live 34; Mismatches
                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 02-JUN-1995
PILING DATE: 25-SEP-1992
PRIOR APPLICATION NUMBER: US 07/951,715
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY AGENT INFORMATION:
                APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.4
Matches 1079; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-459-504B-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1021 VDVQQSHHRSDLVIPEWEAEVSQAVRVCPGCGYILRVTAYKGGYGGCVTIHEIENNTDE 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKFKNCEBEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1162 EBBTYTDVRRDNHÇEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIBIGETBGKFIVDSV 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     925
EDSODLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEMNPDLDCSC
                                                                                                                                                                              RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEBKPLLGEA
                                                                                                                                                                                                                                                                   LSRVKRABKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKL
                                                                                                                                                                                                                                                                                                                                                        VHRIRBAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNYVROGPRINGLACWNVKGH
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APPLICANT: Sutting Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
MONDER OF SEQUENCES: 94
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COMPUTER READABLE FORM:
MEDIUM TYPE: Florm:
COMPUTER: BIBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Desai, Nalini M.
Lewis, Kally S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Bllis J.
Launis, Karen L.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
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|ELLLMEE 1207
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                                                                                                                                                                                NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89;
                      APPLICATION NUMBER: US/08/459,444A
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                                                                                        APPLICATION NUMBER: US 07/951,715
PILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
PILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-459-444-7
                                     FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                            TELEFAX: (919)541-8689
                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS
LENGTH: 1207 amino 8
                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Best Local Similarity
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc. STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
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                                                      721 SEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Croseland, Lyle D.
Wright, Martha S.
Merilin, Ellis J.
Launis, Karen L.
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COMPUTER READABLE FORM:
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US-08-459-444-7
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Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches
        TYPE: amino acide TOPOLOGY: 1:r.
                 SEQUENCE CHARACTERISTICS LENGTH: 1207 amino aci

// MOLECULE TYPE: protein
US-09-053-549-8
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CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQ
                                                               SEHGWWGSENITIQEGNDVFKENYYTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYI
                                                                                 RDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEA
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US-093-549-8

Sequence 8, Application US/09053549

Sequence 8, Application US/09053549

Patent No. 6121521

GENERAL INFORMATION:

APPLICANT: Desat, Nalini

TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121521artis Corporation

STREET: 3054 Cornwallis Rd.

CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
COUNTRY: USA
ZIP: 27709
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/053,549
FILING DATE: 01-APR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: GC 1995
TELECOMMUNICATION INFORMATION:
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Pred. No. 0;
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LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
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US-09-547-422-7
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CITY: Research Triangle Park
STATE: NC
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LSRVRABKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADKL 960
                                                961 VHRIREAYLSELPVIPGVNAEIPEELEGHIITAISLYDARNVVKNGDFNNGLTCWNVKGH
                                                                                                                                                                     EESTYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSV
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OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-APL-2000
CLASSIFICATION **CURROW**
PRIOR APPLICATION NUMBER: US 08/459,595
APPLICATION NUMBER: US 08/459,595
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/72,027
FILING DATE: 04-OCT-1991
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REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:
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481 IPMYKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYRIGPRYASTV
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87.4%; Score 5659.5;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches
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               INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: protein
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO
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US-09-988-462-7
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                                                                     VDVQQSHHRSVLVIPEWBAEVSQAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDE
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER: ISABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRING APPLICATION NUMBER: USAPPLICATION NUMBER: USAPPLICATION NUMBER: USAPPLICATION: ADDRESSED ADDRESSED APPLICATION: ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRESSED ADDRES
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| Patent No. 6720488
| GENERAL INFORMATION:
| APPLICANT: Koziel, Michael G. Besal, Nalini M. Lewis, Kally S. Kramer, Vance C. Warren, Vance C. Warren, Crossland, Lyle D. Wright, Martha S. Merilin, Ellis J. Crossland, Lyle D. Wright, Martha S. Merilin, Ellis J. Italie OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHALL MARKER D. INSECTICIDAL ACTIVITY IN MAIZE
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APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-UN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
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REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
TELEFRAX: (919) 541-8689
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                                                                                                                             LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLN
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                                                                                         961 VHRIREAYLSELPVIPGVNAEIFEELEGHIITAISLYDARNVYKNGDFNNGLTCWNYKGH
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                  LKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTY
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                                                                     VHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVKNGDFNNGLACWNVKGH
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,549
FILING DATE: 01-APR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary W.
REGISTRATION NUMBER: 40,403
REPERENCE/POKET NUMBER: CGC 1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 amino acids
TUDENCE CHARACTERISTICS:
LENGTH: AMINORALEMENTERISTICS:
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APPLICANT: Desai, Nalini
TITLE OF INVENTION: No. 6121521el Insecticic
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121521artis Corporation
STREET: 3054 Cornwallis Rd.
CITY: Research Triangle Park
STATE: NC
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84.3%; Pred. No. 0;
iive 63; Mismatches
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Patent No. 6121521
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Best Local Similarity 84.3
Matches 1040; Conservative
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                    301 V--NWASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT
                                OSRVHVPYYSWTHRSADRTNTISSDSITQIPLYKSFNLNSGTSVVSGPGFTGGDIIRTNV
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Sequence 4, Application US/08176865
Setent No. 5616319
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
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US-08-176-865-4
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                                                                                                                -YTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESNRGYGDYTPLPAGYVTK 1193
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79.9%; Pred. No. 0;
.ive 94; Mismatches 149; Indels
                         1228
                                 ELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1227
                    ELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE
                                                                                       Sequence 4, Application US/08100709
Patent No. 5322687
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ESOLF, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-75-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
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Best Local Similarity 79.9
Matches 983, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-100-709-4
                                                                                                         GENERAL INFORMATION:
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APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CTYET4 AND CTYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBERS OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel Schwarze Jacobs & Nadel c/o A.S.
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ADDRESSEE: Nadel Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel Schwarze Jacobs & Nadel c/o A.S.
ACHTER READALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: 1BM FC Compatible
OSERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: 1BM FC Compatible
OSERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: 1BM FC Compatible
OSERATING SYSTEM: NG/08/176,865
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BEQLIC CATION NUMBER: 276-33
ATTORNEY/AGENT NUMBER: 276-33
REPERROE/DOCKET NUMBER: 276-33
REPERROE/CPOCKET NUMBER: 276-38
REPERROE/CPOCKET NUMBER: 276-38
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80.8%; Score 5237.5; DB 1, Length
Best Local Similarity 79.9%; Pred. No. 0;
Matches 983; Conservative 94; Mismatches 149; Indels
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LENGTH: 1229 amino acids
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TOPOLOGY: linear
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419 RFNFINPQNIYERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLSHIGLII 478
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                                                   QSRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNV
                                                                           GNTLRAPVYSWTHRSADRINTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRIN
                                                                                                                                                       NGSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQ
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                                                                                                                                                                                                                                                           SFRFAEFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVN
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Search completed: November 21, 2004, 17:01:23 Job time : 50 Bec8

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November 21, 2004, 16:55:57 ; Search time 113 Seconds (without alignments) 3848.395 Million cell updates/sec
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1 LTSNRKNBNBIINALSIPAV......IGETEGKFIVDSVELLLMEE 1228
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli	Sequence 38, Appl	Sequence 63, Appl	Sequence 10, Appl	Sequence 7, Appli		6		Sequence 59, Appl	Sequence 2, Appli	7	7	61,
SUMMARIES	US-10-614-524-2	US-10-428-961-38	US-10-428-961-63	US-10-809-953-10	US-09-988-462-7	US-09-826-660-23	US-09-972-175-59	US-10-200-522-59	US-10-855-535-59	US-09-972-175-2	US-10-200-522-2	US-10-855-535-2	US-09-972-175-61
DB	15	14	14	16	10	σ	10	14	17	10	14	11	10
* Query Match Length DB	1228	1228	1227	1228	1207	1186	1189	1189	1189	1189	1189	1189	1189
& Query Match	100.0	8.66	91.3	88.6	87.4	78.8	54.1	54.1	54.1	54.0	54.0	54.0	54.0
Score	6479	6464	5912.5	5742	5659.5	5108	3502.5	3502.5	3502.5	3500.5	3500.5	3500.5	3496.5
Result No.	-	8	٣	4	2	9	7	80	6	10	11	12	13

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DB 15; Length 1228; 0; Indels

100.0%; Score 6479; 100.0%; Pred. No. 0; tive 0; Mismatches

Best Local Similarity 100.0 Matches 1228; Conservative

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TYPE: PRT ORGANISM: Bacillus thuringiensis

; UKGANISM: DO US-10-614-524-2 Query Match 9 9 61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120

1 LISNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 1 LTSNRKNENELINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI

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TITLE R FILE R CURREN CURREN PRIOR PRIOR PRIOR PRIOR PRIOR SEQ ID	TITLE OF INVENTION: Insecticidal FILE REFERENCE: NEWBITSUS2 CURRENT APPLICATION NUMBER: US/10 PRIOR APPLICATION NUMBER: US/09/7 PRIOR APPLICATION NUMBER: US/09/7 PRIOR APPLICATION NUMBER: US/09/7 PRIOR PLIING DATE: 1999-12-19 PRIOR PLIING DATE: 1999-12-28 NUMBER OF SEQ ID NOS: 13 SOFTWARE: Patentin Ver: 2:0 SEQ ID NO 2 LENGTH: 1228	NVENTIONS INVENTIONS IENCE: NEW LICATION DATE ICATION NG DATE: ICATION NG DATE: SEQ ID NG SEQ ID NG SEQ ID NG SECTION NG	CATALLOR DE LA CONTROL DE LA C	icid : US -07- US/0 -19 60/1 0	proteins from Bacillus /614,524 39,243 87	thuringiensis.

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Sequence 38, Application US/10428961

| Sequence 38, Application US/10428961
| Publication No. US20030237111A1
| GENERAL INFORMATION:
| APPLICANT: Baum, James A.
| APPLICANT: Chu, Chih-Rei
| APPLICANT: Chu, Chih-Rei
| APPLICANT: Chu, Chih-Rei
| APPLICANT: Mark J.
| APPLICANT: Mark J.
| APPLICANT: Rupar, Mark J.
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| APPLICANT: Rupar, Mark J.
| APPLICANT: Rupar, Mark J.
| APPLICANT: NECO201-1
| TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
| FILE REFERENCE: MSCO201-1
| CURRENT FILING DATE: 2000-09-13
| FRIOR APPLICATION NUMBER: 09/661,322
| PRIOR FILING DATE: 1999-09-15
| PRIOR FILING DATE: 1999-09-15
| FRIOR FILING DATE: 1999-09-15
| SEQ ID NO 38
| SEQ ID NO 38
| LENGTH: 1228
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99.8%; Score 6464; D
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1224; Conservative 2; Mismatches
                               ETDKVWIEIGETEGKFIVDSVELLLMEE
                                         ; ORGANISM: Bacillus thuringiensis US-10-428-961-38
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                                                                                                                Gaps
                                                                            Length 1227;
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                                                                          DB 14;
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                                                                        91.3%; Score 5912.5;
91.6%; Pred. No. 0;
:ive 36; Mismatches
              ; ORGANISM: Bacillus thuringiensis US-10-428-961-63
                                                                          Query Match
Best Local Similarity 91.64
Matches 1127; Conservative
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Publication No. US20030237111A1

GENERAL INPORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

APPLICANT: Rupar, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Delynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECOZOI--1

CURRENT APPLICATION NUMBER: 09/661,322

PRIOR APPLICATION NUMBER: 00/661,322

PRIOR PLIING DATE: 2000-09-13

PRIOR PLIING DATE: 1999-00-15

NUMBER OF SEQ ID NOS: 63

SEQ ID NO 63

LENGTH: 1227
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                                                                                      PAEPPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFRABYDLERAQEAVNALF
                                                                                                              FTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVPKENYVTLPGTFNECY
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Db 296 VNMASMNWNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNITHMTVWRGHTIQ 355 Oy 361 SRPIGGGLATSTHGSTATSINPVRLSFPSRDVWTESYAGVLLWGIXLEPIHGVPTVRFN 420 Db 356 SRPIGGGLATSTHGATNTSINPVRLSFPSRDVWTESYAGVLLWGIYLEPIHGVPTVRFN 415 OY 421 FRNPQNFPERGTANYSOPYESPGLGLKDSETELPPETTERPNYESYSHRLSHIGLISOSR 480 1		Db 1016 SLYDARNVKNORPHINIT
	RESULT 4 US-10-809-953-10 Sequence 10, Application US/10809953 Publication No. US20040191825A1 GENERAL INFORMATION: APPLICANT: Van Mellact, Herman APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, Johan APPLICANT: Van Mellact, US/10/809,953 CURRENT FILING DATE: 2004-03-26 FRIOR PILING DATE: 1090-05-30 FRIOR PILING DATE: 1090-05-31 FRIOR PILING DATE: 1990-05-30 FRIOR APPLICATION WUMBER: GB 89401499.2 FRIOR PILING DATE: 1990-05-31 NUMBER OF SEQ ID NOS: 10 SEQ ID NO 10 LENGTH: 1228 TYPE: PRT ORGANISM: Bacillus thuringiensis US-10-809-953-10 QUETY Match Best Local Statlacter ORGANISM: Best Local Statlacte	Fred. No. 0; Wisherd Mo. 0; Wisherd Moles 10; Gaps 3; Wisherd Moles 10; Gaps 3; Wisherd Moles Poar Indels 10; Gaps 3; Wisherd Moles Moles Moles 10; Gaps 3; Wisherd Moles Mole

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745 720 805 865 840

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Patent No. US20010026940A1
GENERAL INFORMATION:
APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
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           Evola, Stephen'v.

Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INVENTION: SYNTHETIC DA ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89; Indels
                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. US20030046726A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422
FILING DATE: 11.APP.2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-UNN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-CCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                       NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.4%; Score 5659.5;
89.4%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Mismatches
                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3054 Comwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
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Warren, Gregory W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEFAX: (919)541-8689
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Matches 1079; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/337,635
FILING DATE: «INKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
                              718 PNFRGINROLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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US-09-972-175-59
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## APPLICANT: Narva, Kenneth B.

## TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
## FILE REPERENCE: Ma-714XC2D1

## CURRENT APPLICATION NUMBER: US/09/826,660

## CURRENT FILING DATE: 2001-04-05

## PRIOR APPLICATION NUMBER: 09/178,252

## PRIOR APPLICATION NUMBER: 60/065,215

## PRIOR APPLICATION NUMBER: 60/065,215

## PRIOR APPLICATION NUMBER: 60/076,445

## RIOR RILING DATE: 1998-03-02

## NUMBER OF SEQ ID NOS: 27

## SEQ ID NO 23

## LENGTH: 1186
                                                                                                                                                                                                                                                                                                                        NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDOWEJFLEHVEQLINQQITENARNTA
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                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                        Length 1186;
                                                                                                                                                                                                                                 Query Match 78.8%; Score 5108; DB 9; Length 1 Best Local Similarity 80.6%; Pred. No. 0; Matches 995; Conservative 76; Mismatches 108; Indels
                                                                                                                                                                                                        gene
                                                                                                                                                                                                 OTHER INFORMATION: Toxin encoded by synthetic B.t.
                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Seguence
                                                                                                                                                                                                              US-09-826-660-23
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        778
                                                                                                        839 ESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDGCTDLHENLGVWVV 898
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PNFTSINKOPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNE
                                                                                                                                                                                                                                                                       CYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV
                                                                                                                                                                                         820 PSPIG-------KCAHHSHHFSLDIDVGCTDLNEDLGCWVI
                                                                                                                                                                                                                                                 PKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTBAKEAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application US/09972175
Publication No. US20030101482A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
Gilmer, Amy Jelen
Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
EPPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1194 KELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIF: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-Oct-2001
CLASSIFICATION: <UNKNOWN>
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                   TNAASWVRYNOFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304
                                                                                                                                                                                                                                                                                                                                                                               SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364
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                                                                                                          Query Match 54.1%; Score 3502.5; DB 10; Length 1189; Best Local Similarity 57.0%; Pred. No. 1.6e-262; Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps
                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: 59:
        INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TELEFAX: 512/474-7577
                                                                                     US-09-972-175-59
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JOHNSTON AND ALLOCATION JAMES A.

JAPPLICANT: Baum, James A.

APPLICANT: Gilmer, Anne Marie Light
APPLICANT: Mettus, Anne Marie Light
APPLICANT: Mettus, Anne Marie Light
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-T
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: MECO:213 (11792.0213 DVUSO1)
CURRENT APPLICATION NUMBER: US/10/200,522
FRIOR APPLICATION NUMBER: 09/337,280
PRIOR APPLICATION NUMBER: 09/397,210
PRIOR APPLICATION NUMBER: 09/980,071
PRIOR APPLICATION NUMBER: 08/757,536
PRIOR APPLICATION NUMBER: 08/757,536
PRIOR APPLICATION NUMBER: 08/757,536
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PRIOR
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                                                   HFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKK
                                                                                                                                                                                                            WRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS
HHFSLDIDIGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK
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US-10-200-522-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 59, Application US/10200522; Publication No. US20030195336A1; GENERAL INFORMATION:
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us-10-614-524-2.rapb

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JOURNALL INFORMATION:

JAPPLICANT: Baum, James A.

APPLICANT: Gilmer, Amy Jelen

APPLICANT: Gilmer, Amy Jelen

APPLICANT: Gilmer, Amne Marie Light

TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides

TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides

TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides

TITLE OF INVENTION: AND MARIER: US/10/855,535

CURRENT APPLICATION NUMBER: US/10/855,535

PRIOR APPLICATION NUMBER: 08/390,071

PRIOR APPLICATION NUMBER: 08/390,071

PRIOR PILING DATE: 1995-11-27

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.2

LENGTH: 1189
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Best Local Similarity 57.0%; Pred. No. 1.6e-262;
Matches 717; Conservative 143; Mismatches 289; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Recombinant Delta Endotoxin
US-10-855-535-59
                   Sequence 59, Application US/1085533
Publication No. US20040221334A1
GENERAL INFORMATION:
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                                       TNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMA 304
                                                                      SMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPI 364
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RESULT 9 US-10-855-535-59

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RILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTALARL 124
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nlarity 57.0%; Pred. No. 2.4e-262;
Conservative 143; Mismatches 289;
                NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                                                                                                                                                      TYPE: amino acidd
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-972-175-2
                                                                                                                                                                                                                                                                               Similarity
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                                                                                              KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN
                                                  612 IILADATFEAESDLERAQKAVNALFTSSNOIGLKTDVTDVHIDOVSNLVDCLSDEFCLDE
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Gilmer, Amy Jelen
Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTE EXPRESSING
LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
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MEDIUM TYPES: Floppy disk

COMFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 05-Oct-2001

CLASSIPICATION: CUNKNOWN>

PRIOR APPLICATION: AUNKNOWN>

PRIOR APPLICATION: AUNKNOWN>

FILING DATE: «UNKNOWN>

FILING DATE: «UNKNOWN>

FILING DATE: «UNKNOWN>
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STREET: P.O. Box 4433
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Publication No. US20030101482A1
GENERAL INFORMATION:
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STATE: Texas
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US-09-972-175-2
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Mettus, Anne-Marie Light
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
       RTINVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-
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Publication No. US20040221334A1
Sequence 2, Application US/1085535
Publication No. US20040221334A1
GABERAL INFORMATION:
APPLICANT: Balum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne Marie Light
TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides
TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides
TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides
TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides
TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides
TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides
CURRENT APPLICATION NUMBER: 08/131/635
PRIOR FILING DATE: 1999-66-21
PRIOR FILING DATE: 1999-11-26
PRIOR PILING DATE: 1999-11-26
PRIOR PILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 76
SOFTWARRE: Patentin version 3.2
SOFTWARRE: Patentin version 3.2
SOFTWARRE: Patentin version 3.2
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NONOCIPYNCLS-----SIDISLSLVQ 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRATURE:
; OTHER INFORMATION: Recombinant Delta Endotoxin US-10-855-535-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1189
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TWEIGENLTSRTFRYTDFSNPFSFRANPDIIGISEQPLFGAG-SISSG----ELYIDKIE 611
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          FILING DATE: 05-0ct-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/337,635
FILING DATE: «Unknown»
ATORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
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APPLICATION NUMBER: US/09/972,175
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
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Sequence 61, Application U8/10200522
Fublication No. US20030195336A1
GENERAL INFORMATION:
APPLICANT: Bulm, James A.
APPLICANT: Bulmer, Amy Jelen
APPLICANT: Martus, Anne Marie Light
TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-TC,
TITLE OF INVENTION: WOLKER ACID AND POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-TC,
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: MECO.213 (11792.0213 DVUS01)
CURRENT FILING DATE: 2002-07-22
CURRENT FILING DATE: 2002-07-22
FRIOR PELICATION NUMBER: 09/337,280
FRIOR PELICATION NUMBER: 08/380,071
FRIOR PLLING DATE: 1997-11-26
FRIOR PLLING DATE: 1996-11-27
FRIOR FILING DATE: 1996-11-27
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TYPE: PRT
ORGANISM: Artificial Sequence
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 ----SSIDISLSLVQ 43
                                                                                                                                              220 STYQDWITYNRLRRDLTLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPL----INFN
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                                                                                                                                                                                      276 PQLQSVAQLPTFNVMESSAIRNPHLFDILNNLTIFTD---WFSVGRNFYWGGHRVISSLI
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                                                        QGLGDSPRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMV
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Sequence 61, Application US/10855335

Sequence 61, Application US/10855335

Publication No. US20040221334A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Baum, James A.

APPLICANT: Baum, James A.

APPLICANT: Mettus, Anne Marie Light

TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides

TITLE OF INVENTION: and Methods of Use (Amended)

FILE REFERENCE: 11792.0214.DVUS02

CURRENT APPLICATION NUMBER: US/10/855,535

CURRENT PILING DATE: 1999-06-21

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PRIOR PELING DATE: 1996-11-27

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.2

SES DE NO NO 61

TEMBER OF SEQ ID NOS: 76
EVYPTDTGTCNDYTA----HQGTAVCNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDVR 1170
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                           1074 EVYPNNTVTCNNYTGTQEEYEGT--YTSRNQGYDEAYGNNPSVPADYASVYEEKSYTDGR
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393TPTNSFTYRGRGTVDSLTELPPEDNSVPPREGYSHRLCHATFVQ 436	478 QSRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII 533	437 **GTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL 496		ARVIVLTGAASTGVGGQVSVNMPLQK 55		THE GENLISSTFRYIDESNPESFRANPDIGISEQPLEGAG-SISSGELYIDKIE 61		512 IILADATFEAESDLERAQKAVNALFISSNQIGLKTDVTDYHIDQVSNLVDCLSDEFCLDE 671		572 KRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDRGWRGSTD 713		ITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEIYL	IRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHS	74 IRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS 833	w		WEDKREKLOLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLS	WEDKREKLQLETNI VYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRIREAYLP		** ELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDVEEQNNHR	S SVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKBGYGEGCVTIHEIENNTDELKFKNCEEE	SVLVIPEWEAEVSQEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEE	ın		RDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE 12	
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Search completed: November 21, 2004, 17:04:22 Job time : 119 secs

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November 21, 2004, 16:50:34; Search time 43 Seconds (without alignments) 2747.772 Million cell updates/sec Run on:

US-10-614-524-2 6479 1 LTSNRKNENBIINALSIPAV......IGETEGKFIVDSVELLLMEB Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008.
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	parasporal crystal	_	_	_	_	Ä	ä	٦	Н	_	٦	Ä	_	٦	Ä	_	٦	٦	parasporal crystal	Ä	Ä	_	_	٦	_	_	parasporal crystal	cryv465 protein -	
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	Score	5745	3791	3484.5	3433.5	3433	3426.5	3421	3413.5	3413.5	3412.5	3411	3405.5	3400.5	3399.5	3399.5	3399	3387	3323.5	3283	3269	3268	3257.5	3251	3161.5	2434	2294.5	2200.5	2170.5	2110
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ALIGNMENTS

	thuringiensis	
ESULT 1 00873	parasporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis	Alternate names: parasporal crystal protein cryA4
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C;Species: Bacillus funcingiensis subspicatory para processis secies: Bacillus funcingiensis subspicatory by the sequence revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
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Gaps 10; Length 1228; 90; Indels Query Match 88.7%; Score 5745; DB 2; Best Local Similarity 89.1%; Pred. No. 0; Matches 1098; Conservative 35; Mismatches 90; 9 55 1 MTSNRKNBNBIIN----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 1 LISNRKNENELINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI ઠ g

61 NIAGRILGVLGVPFAGQIASPYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 120 56 NIAGRILGVLGVPFAGQLASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA 115 ò 셤

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       FGPIRVTVNGPLTQRYRIGFRYASTVDFDFFVSRGGTTVNNFRPLRTMNSGDELKYGNFV
                                                                       FAEFPVGISASGSO-TAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAGEAVNAL
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C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48970
R;Kalman, S: Kiehne, K.L.; Libbs, J.L.; Yamamoto, T.
Appl. Environ. Microbiol. 59, 1131-1137, 1993
A;Title: Cloning of a novel crylC-type gene from a strain of Bacillus thuringien A;Reference number: A48970; MuID:93236401; PMID:8476286
A;Accession: A48970
A;Accession: A48970
A;Accession: A48970
A;Accession: A48970
A;Cross-references: UNIPROT:P56953; GB:M97880; NID:g289263

16; 153 213 188 248 333 304 69 334 EQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVY 393 305 NNLTIFTD---WESVGRNFYWGGHRVISNRIGGGNITSPIYGREANQEPPRSFTFNGPVF 361 405 488 451 548 511 609 571 668 728 631 691 788 733 848 793 908 853 968 RDQWEIFLEHVEQLINQOITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSV 40 CIAEGNNINPLVSASTVQTG---INIAGRILGVL---GVPFAGQIASFYSFLVGELMPRG LYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDAŞLFGSEFGLTSQEI QRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLDLVALFPS YDTRTYPINTSAQLTREVYTDAIGATGVNWASMNWYNNNAPSFSAIETAVTRSPHLLDFL 249 YDNRRYPIQSVGQLTREIYTDPLITFNPQLQSV----AQLPTFNVMESNAIRTPHLFDVL (NCBIN:129672, NCBIP:129675) 433 ANYSQPYESPGLQLKDSETELPPETTERPNYESYSHRLSHIGLISQSRVHV----PVYSW V------DSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGPVFSW THRSADRINTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNF 394 WIESYAGVLIMGIYLEPIHGVPTVR------FN-----FRNPQNTFE---RGT NNTSLORYRVRYRAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGI SASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEYDLERAQEAVNALFTNTNPRRL KTDVTDVHIDQVSNLVACLSDEFCLDEKRELLEKVKVAKRLSDERNLLQDPNFTSINKQP DFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKI GESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEP NRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDJDJGCTDLHENLGVWVVFKIKTQEGHA RLGNLEFTEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYN Length 1176; Indels Query Match 58.5%; Score 3791; DB 2; Best Local Similarity 62.3%; Pred. No. 3.9e-233; Matches 762; Conservative 125; Mismatches 241; A;Experimental source: subsp. galleriae HD29 A;Note: sequence extracted from NCBI backbone C;Superfamily: parasporal crystal protein C;Keywords: delta-endotoxin 94 154 214 189 274 406 489 549 609 572 699

us-10-614-524-2.rpr

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parasporal crystal protein crylDal - Bacillus thuringiensis
NyAlternate names: parasporal crystal protein crylD
NyAlternate names: parasporal crystal protein crylD
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Accession: S11446
C;Accession: S11446
N;Hoeffer, H.; Soetaert, P.; Jansens, S.; Peferoen, M.
Nucleic Acids Res. 18, 5545, 1990
A;Title: Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specif
A;Reference number: S11446
A;Reference number: S11446
A;Residus: prellminary
A;Molecule type: DNA
A;Residues: 1-1165 A;MCB
A;Residues: 1-1165 A;MCB
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHFSLDIDIGCTDLHENIGVWVVPKIKTQEGHARLGNLEFIEEKPLLGEALSRVKRAEKK 935
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                                QSRVHV---; PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDII
                                                                                              RTINVNGSVLSMGLNFNNTSLQRYRVRVRYAASQ-----TMVLRVTVGGSTTFDQGFPS
                                                                                                                                                                                                                                                                                    KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSEN
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                                                             RSGTPFLTTGVVPSWTDRSATLTNTIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDIL
                                                                                                                                                                                                                        FIPITATFEAEYDLERAQEAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEPCLDE
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C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: 800944
R;Honee, G.; van der Salm, T.; Visser, B.
Nucleic Acids Res. 16, 6240, 1988
A;Title: Nucleotide sequence of crystal protein gene isolated from B. thuringiensis subs A;Reference number: 800944, MUID:88289380; PMID:3399402
A;Accession: 80094
A;Status: translation not shown
A;Residues: 1-1189 <HON>
A;Residues: 1-1189 <HON>
A;Residues: 1-1189 cHON>
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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RLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVV
                                                            100 EGLGNNFNIYVEAPKEWEEDPNNPETRTRVIDRFRILDGLLERDIPSFRISGFEVPLLSV
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                     914 RLQADTNIAMIHAADKRVHRIREAYLPELSVIPGVNAGIFEELEGRIFTAYSLYDARNVI
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Best Match	Best Local Similarity 57.4%; Pred. No. 2.4e-210; Media 1165; Matches 703; Conservative 141; Mismatches 273; Indels 107; Gaps 22;	අ ල	964 NGI
ò	VSASTVOTGINIAGRILGVLGVPFAGQIASFYSFLVGE	ò	1089 YGE
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e e		qa	: 1082 EAY
ò		ò	1205 VWI
QQ		<u>අ</u>	1142 VWI
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ò		C,Specie	es: Baci
qq	SYPTFSAAESAIIRSP	C, Accession: 8326 R; Lambert, B.	sion: 83; ct. B.
ò	328 HLLDFLEQLTIFSTS-SRWSATRHWTYWRGHTIOSRPIGGGLNTSTHGSTNTSINPV 383	Submitte A;Refere	ad to the
QQ	298 HLVDFLNSFTIYTDSLARYAYWGGHLVNSFRTGTTTNLIRSPLYGREGNTERPV 351	A, Access	ion: S3
ò	384 RLSFF-SRDVYWTESYAGVILMGI-YLEPIHGVPTVRFNFRNPQNTFERGTANVSQPYES 441	A, Molect A, Residu	le type
e G	TLSYITGLDNSNP	A;Cross-C;Superf	referenciamily:
ò		C; Keywor	ds: delt
og G		Query Best 1	Query Match Best Local Simil
ò	499 ISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIRTNVNGSVLSMGLNFNNTSLQRYRV 558	Matche	1 693;
ପ୍ପ		è	54 STVC
ờ	559 RVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQ 614	đ	34 SQVS
qq	515 RFRYASVANRSGTFRYSQPPSYGISFPKTWDAGBPLTSRSFAHTTLFTPITFSRAQEE 572	ò	114 ENAR
ò		qa	88 ELER
Db		'n	174 IRNO
ò		qa	148 IRNL
qq		%	234 WYNT
ò	730 FISTNEQSNPTSIHEQSEHGWMGSENJTIQBGNDVFKENYVTLPGTFNECYPTYLYQKIG 789	qa	208 WYNQ
QQ		ð	294 DAIG
È		ଶ୍ର	264 SPVV
Q _Q		ò	354 WRGH
ò		q	306 WAGH
qq		ò	407 YLEP
ò	910 LGNLEFIEEKPILGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNR 969	qq	366 89001
QQ		à ·	
රු ස්	970 LQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYDARNVVK 1029	අ දි	414 SHRL
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es: UNIPROT:045746; EMBL:222510; NID:g295861; PIDN:CAA80233.1; PID:g29586
arasporal crystal protein
a-endotoxin
DFINIGLACWIVKGHVDV-QQSHHRSVLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEG 1088
                 EGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTA----HQGTAVCNSRNAGYE 1144
                                                                         YEVDTTASVNYKPTYEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEYFPETDK 1204
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lus thuringiensis
998 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
645
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.larity 57.9%; Pred. No. 2.5e-210;
.Conservative 137; Mismatches 281; Indels 86;
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                                                                                          STNTSINPVRL-SFFSRDVYWTES---YAGVLLWGIYLEPIHGVPTVRFNFRNPQNTFER
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                                 LEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNGEVPLLMVYAQAANLHLLLLR
                                                                            DASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQFR
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parasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)
parasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)
C;Species Bacillus thuringiensis
C;Species Bacillus thuringiensis
C;Accession: A41052
R;Lee, C.S.; Aronson, A.I.
J Bacteriol. 173, 6635-6638, 1991
A;Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp. A;Reference number: A41052; MUD: 92011442; PMID: 1655719
A;Accession: A41052
A;Accession: A41052
A;Accession: A41052
A;Accession: A1052
A;Accession: A1052
A;Accession: A1052
A;Cross-references: UNIPOT: Q03748; GB: M65252; NID: g142874; PIDN: AAA22410.1; PID: g142875
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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Parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)

N.Alternate names: 135K insecticidal protein

N.Alternate names: 135K insecticidal protein

C.Species: Bacillus thuringiensis

C.Species: Bacillus thuringiensis

C.Sacession: JT0241

R.Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.

Agric: Biol. Chem. 52, 1565-1573, 1988

A.Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein

A, Reference number: JT0241

A, Molecule type: DNA

A, Molecule type: DNA

A, Residues: 1-1176 - SHI>

A, Molecule type: DNA

A, Residues: 1-1176 - SHI>

A, Cross-references: UNIPROT: P02965

A, Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein

C, Superfamily: parasporal crystal protein

C, Superfamily: parasporal crystal protein

C, Superfamily: parasporal crystal protein
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submitted to the EMBL Data Library, April 1993
A,Reference number: S32645
A,Rocession: S32647
A,Status: preliminary
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C,Superfamily: parasporal crystal protein
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                                                                                                              atch 52.6%; Score 3411; DB 2; Length 1160; cal Similarity 56.2%; Pred. No. 6.3e-209; 695; Conservative 145; Mismatches 288; Indels 108;
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paragporal crystal protein crylAa - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
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C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
B;Udayasuriyan, U; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
B;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
B;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
B;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
B;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
B;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mori, H.; Mor
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                                                828 GVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLELETNIVYKE
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                                                     396 NLPSTIYRQRGTV-------DSLDVIPPQDNSVPPRAGFSHRLSHVTMLSQAA
                                                                        ----RVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPFTGGDIIRT
                                                                                     GAVYTLRAPTFSWQHKSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILFR
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                                                                                                                       SQSFRFAEFPVGIS-ASGSQTAGISIS-NNAGRQTFHFDXIEFIPITATFEAEYDLERAQ
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                                    --PONTF-ERGTANYSOPYESPGLOLKDSETELPPETTERPNYESYSHRLSHIGLISQS-
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Databour 13 Darasporal crystal protein cryA - Bacillus thuringiensis (strain entomocidus) Cispecies: Bacillus thuringiensis Cibate: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004 CiAccession: 502215 RiMasson L.; Marcotte, P.; Prefontaine, G.; Brousseau, R. Nucleic Acids Res. 17, 446, 1989 A;Title: Nucleotide sequence of a gene cloned from Bacillus thuringiensis subspecies A;Reference number: 502215; MUID:89098405; PMID:2911478 A;Status: translation not shown

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EMBL:X13535; NID:940266; PIDN:CAA31886.1; PID:940267 24; 136 112 SLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLL 196 172 256 232 316 280 370 335 423 479 441 501 595 561 653 620 713 680 833 77 55 773 722 842 782 893 953 27 MDLSPDARIEDSLCIAEGNNINP---LVSASTVQTG---INIAGRILGVL---GVPFAGO IASFYSFLVGELWP-RGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQ ---FVLGLVDIIWGIFGPSQWDAFPVQIEQLINQRIEBFARNQAISRLEGLSNLYQIYAE || :|: || MDNNPNI----NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG-SAIETAV---IRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQSRPIGGG---LNT STHGSTNTSINPVRLSFFSRDVYWTES---YAGVLLW-GIYLEPIHGVPTVRFNFRN---NVNGSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLT RDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGLNSLRGTNAASWVRYNQF RRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVYTDAIGATGVNMASMNWYNNNAPSF 336 PLFGNAGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTT GAVYTLRAPTFSWQHRSAEFNNIFSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRR TSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQ SQSFRFAEFPVGIS-ASGSQTAGISIS-NNAGRQTFHFDKIEFIPITATFEAEYDLERAQ BAVNALFTINTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDER |||||||| ||:| | |NLLQBPNFRGINRQLD-------RGWRGSTDITIQGGDDVFKENYVTLL --PONTF-ERGTANYSOPYESPGLOLKDSETELPPETTERPNYESYSHRLSHIGLISOS-----RVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRT NLLODPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKENYVTLP GTFNECYPTYLYQKIGESELKAYTRYQLRGY1EDSQDLEIYLIRYNAKHETLDVPGTESV WPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEXCAHHSHHFSLDIDIGCTDLHENL GVWVVFKIKTQEGHARLGNLEFIBEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTE Gapa 1176; 100; Length Indela / Match 52.5%; Score 3400.5; DB 2; Local Similarity 56.2%; Pred. No. 3e-208; Nes 696; Conservative 149; Mismatches 294; A,Molecule type: DNA
A,Residues: 1-1176 <MAS>
A,Cross-references: UNIPROT:P02965; EMBL:X
C,Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin 78 173 Query Match 99 113 197 257 317 371 424 396 480 536 502 621 442 295 654 714 681 774 723 834 394 843 Best Loca Matches ò ద δ 셤 ठे g ò a ò 셤 g Š ò 셤 ò g ઠે g 8 6 8 6 8 8 8 셤 충 <u>염</u> 8 6 8 6

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parasporal crystal protein crylAc1 [validated] - Bacillus thuringiensis subsp. kurstaki parasporal crystal protein crylAc1 [validated] - Bacillus thuringiensis subsp. kurstaki C;Species: Bacillus thuringiensis subsp. kurstaki C;Species: Bacillus thuringiensis subsp. kurstaki C;Species: Bacillus thuringiensis subsp. kurstaki C;Date: 18-Apr-1984 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004 C;Accession: A23962; A03489 R;Adang M.J.; Staver, M.J.; Rocheleau, T.A.; Leighton, J.; Barker, R.F.; Thompson, D.V. Gene 36, 289-300, 1985 A;Title: Characterized full-length and truncated plasmid clones of the crystal protein o A;Reference number: A91526; MUID:86083171; PMID:3000881 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 A;Accession: A23962 
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                                    ----RVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRT
                                                                                                                                      GAVYTLRAPTFSWQHRSABFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRR
                                                                                                                NVNGSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLT
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A22617
Bacasporal crystal protein crylAal - Bacillus thuringiensis
C;Bacies: Bacillus thuringiensis
C;Bacies: Bacillus thuringiensis
C;Accession: A22617
C;Accession: A22617
C;Accession: A22617
B;Schnepf, H.E.; Wong, H.C.; Whiteley, H.R.
J. Biol. Chem. 260, 6264-6272, 1985
A;Title: The amino acid sequence of a crystal protein from Bacillus thuringiensis deduce
A;Reference number: A22617
A;Reference number: A22617
A;Residues: 1-1176 <SCAT
A;Residues: 1-1176 <SCAT
A;Residues: 1-1176 <SCAT
CCOSSE-references: UNDRN
C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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A;Title: Transcriptional and translational start sites for the Bacillus thuringiensis cr
A;Reference number: A92410; MUID:83109004; PMID:6296116
A;Accession: A03103
A;Accession: A03103
A;Residues: 1-76, 'P', 78-147, 'L',149-247,'S',249-282,'M',284-285,'R',287-288,'QN',291-292
A;Experimental source: strain HD-1
C;Comment: This protein is present in crystalline form as a component of the spore coat.
C;Superfamily: parasporal crystal protein
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                                                                                                                                                                                                               --FVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAE 112
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                                                                                                            Ouery Match 52.5%; Score 3399.5; DB 1; Length 1178; Best Local Similarity 56.7%; Pred. No. 3.5e-208; Matches 704; Conservative 148; Mismatches 287; Indels 102;
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completed: November 21, 2004, 17:02:15 e : 47 Becs Search cor Job time

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 21, 2004, 09:24:41; Search time 153 Seconds (without alignments) 4618.040 Million cell updates/sec Run on:

US-10-614-524-2 6479 1 LTSNRKNENEIINALSIPAV.....IGETEGKFIVDSVELLLMEE 1228 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 1825181 segs, 575374646 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMEDIES

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J	Query Match	91.4	88.7	88.6	88.5	80.8	80.5	80.1	76.5	66.1	61.4	60.2	60.2	58.5	55.2	54.9	54.0	54.0	54.0	54.0	53.8	53.3	53.0	53.0	52.9	52.9	52.9	52.9	52.9	52.9	52.8	52.7
	Score	5924.5	5745	5740	5737	5235.5	5214.5	5188.5	4959.5	4284.5	3977.5	3901.5	3901.5	3791	3579	3556	3495.5	3495.5	3495.5	3495.5	3485.5	3455.5	3433.5	3433	3428	3426.5	3426	3426	3426	3425	3421	3413.5
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BACTU C1BE BACTU STANDARD; PRT; 1227 AA. 085805; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 44, Last sequence update) 05-JUL-2004 (Rel. 44, Last sequence update) Pesticidial crystal protein crylBe (Insecticidal delta-crylEo; Synonyms-crylBe (Insecticidal delta-blasticidial crystaline entomocidal protoxin) (139 kDa cr. Name-crylBe; Synonyms-crylB(e), 158C2B; Bacillus thuringiensis. Bacillus thuringiensis. Bacillus thuringiensis. Bacillus thuringiensis. Bacillus thuringiensis. Bacillus thuringiensis. CSTAINENER B-18872 / PS158C2; STAINENER B-18872 / PS158C2	EMBL, AF077326, AAC32850.1; HSSP, P07130; IDLC. InterPro; IPR00178; Endotoxin. InterPro; IPR005638; endotoxin.C. InterPro; IPR008979; Gal.bind Iike Pfam; PF03944; Endotoxin C; 1. Pfam; PF03945; Endotoxin M; 1. Pfam; PF03945; Endotoxin M; 1. Pfam; PF03945; Endotoxin M; 1. Pfam; PF03945; Endotoxin M; 1. Pfam; PF03945; Endotoxin M; 1. Pfam; PF03945; Endotoxin M; 1. Pfam; PF03945; Endotoxin M; 1. Pfam; PF03945; Endotoxin M; 1. Pfam; PF03945; Endotoxin M; 1. Pfam; PF03945; Endotoxin M; 1.	4.4
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T 1 CIBE BACTU STAN CIBE BACTU G8885; 16-OCT-2001 (Rel. 4) G9-OCT-2001 (Rel. 4) G9-UL-2004 (Rel. 4) G9-UL-2004 (Rel. 4) FPERTICIDAL CYPERIN Name=CYIBE; Synony Bacillus thuringien Bacteria; Frrancute NCBI TAXID=1428; IL	AF077326, AAC AF077326, DLC. rc; IPR001178 rc; IPR005638 rc; IPR008639 rc; IPR008979 PF03944; Endo PF03955; Endo A, Sporulatio	<u> </u>
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                                                         RNAGYEDAYEVDTTASVNYKPTYEEETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithalial cells of insects.
--- EDVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part the spore coat.
--- MISCELLANBOUS: Toxic segment of the protein is located in the N-
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89.1%; Pred. No. 0;
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SPECIES=B.t.entomocidus; STRAIN=HD-110;
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InterPro; IPR005638; endotoxin.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal bind Tike.
Pfam; PP00555; Endotoxin.C; 1.
Pfam; PP00555; Endotoxin.M; 1.
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Best Local Similarity 89.1:
Matches 1098; Conservative
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Qy 1080 LRVTAYKEGYGEGCVTIHEIENNTDELKFKNCEEE DD 1076 LRVTAYKEGYGEGCVTIHEIENNTDELKFKNREEE Qy 1136 CNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDW DD 1136 CNSRNAGYEDAYEVDTTASVNYKPTYEEETYTDW Qy 1196 LEYPPETDKVWIEIGETEGKFIVDSVELLLMEE DD 1196 LEYPPETDKWIEIGETEGKFIVDSVELLLMEE DD 1196 LEYPPETDTWIEIGETEGKFIVDSVELLLMEE	SULT 3 3175 Q93175; Q93175; Q93175; Q1-DEC-20 O1-DEC-20 O1-DEC-20 O1-MAR-20 DELta-end Name=cryla; NCEL TaxI [1] SEQUENCE STRAINS MA MAT INS MA HSSP; AN3 HSS	Db 296 VNMASMNWYNNNAPSFSAIEAAAIRSPHLLDFLEC Qy 361 SRPIGGGLNTSTHGSTNTSINFVRLSFFSRDVYWT
1 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60	·	1016 SLYDARNVKNGDFNNGLTCWNVKGHVDVQOSHHRSDLVIPEWEAEVSQAVRVCFGCGYI 1075
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296 VNWASMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGRTIQ 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA
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89.0%; Pred. No. 0;
ive 35; Mismatches 91; Indels 10
          Best Local Similarity 89.08 Matches 1097; Conservative
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                           FRNPONTFERGTANYSOPYESPGLOLKDSETELPPETTERPNYESYSHRLSHIGLISQSR
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Q93NM5 Q93NM5 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CrylBa.
Name=crylBa,
Bacillus thuringiensis.
Bacillus thuringiensis.
Bacillus taxingiensis.
NCBL TaxID-1428;
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YPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVE
                       YPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVE
                                                                              SPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVF
                                                                                                     SPIGECGEPURCAPHFEWNPDLDCSCRDGEKCAHISHHFSLDIDVGCTDLHENLGVWVVF
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylBb (Insecticidal delta-endotoxin
CrylB(b) (Crystaline encomocidal protoxin) (140 kDa crystal protein)
Name-crylBb; Synonyme-crylB(b), crysT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=NRRL B-21110 / EG5847;

Donovan W.D., Tan Y.C.S., Gonzalez J.M. Jr.;

Donovan W.D., Tan Y. Jany C.S., Gonzalez J.M. Jr.;

Donovan W.D., Tan Y. Jany C.S., Gonzalez J.M. Jr.;

Donovan W.D., Tan Y. Jany C.S., Gonzalez J.M. Jr.;

Patent number US3322687, 21-JUN-1994.

-1- FUNCTION: Promotes colloidosmocio lysis by binding to the midgut epithelial cells of many lepidopteran larvae.

-1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.

-1- MISCELLANBOUS: Toxic segment of the protein is located in the N--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis.
Bacceria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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                                                                         Pfam; PF03944; Endotoxin_C; 1.
Pfam; PF00555; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
Sporulation; Toxin.
SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                               80.8%; Score 5235.5;
79.8%; Pred. No. 0;
ive 95; Mismatches
IPR005639; endotoxin_N.
IPR008979; Gal_bind_like
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Local Similarity 79.7%
les 987; Conservative
                  1231 AA;
         Toxin.
        Sporulation;
SEQUENCE 12
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              AISLYDARNVVRNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVSQAVRVCPGRG
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pesticidal crystal and annotation update)
CrylB(d)) (Crystaline entomocidal protoxin) (140 kDa crystal protein)
Name-crylB(3, Synonyms-crylB(d), cryLAl, cryBl;
Bacillus thuringiensis (subsp. wuhanensis).
NGB Asillus firmicutes; Bacillales; Bacillus.
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DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F., "Cloning of two new cry genes from Bacillus thuringiensis subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wuhanensis strain.";
Curr. Microbiol. 40:227-232(2000).
-1- FUNCTION: Promotes colloidosmotic lysis by binding to the mepithelial cells of lepidopteran larvae. Toxic to Plutella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        terminus.
SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                 YPPETDKVWIEIGETECKFIVDSVELLIMEE 1228
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Interpro; IPR005639; endotoxin C.
Interpro; IPR005639; endotoxin N.
Interpro; IPR008979; Gallbind Inke.
Pfam; PF03944; Endotoxin C; IPfam; PF03945; Endotoxin M; I.
Pfam; PF03945; Endotoxin M; I.
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MEDLINE=20153386; PubMed=10688690;
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                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                         NIAGRILGVLGVPFAGQIASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNTA
                                                                                                                                                                                                               LARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVP
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                                                               17;
                                 Length
                                                               Indels
139654 MW; 129A0371CDDBEE52
                                 DB 1;
                                           79.7%; Pred. No. v,
tive 94; Mismatches 140;
                            80.5%; Score 5214.5; 79.7%; Pred. No. 0;
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                                                                                                                  GNTLRAPVYSWTHRSADRINTIGPNRITQIPAVKGRFLFNG-SVISGPGFTGGDVVRLNR
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  V--NWASMNWYNNNAPSFSAIETAVIRSPHLLDFLEOLTIFSTSSRWSATRHMTYWRGHT
                                                    IQSRPIGGGLNTSTHGST-NTSINPVRLSFFSRDVYWTESYAGVLLWGIYLEPIHGVPTV
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(Rel. 39, Last sequence update)
(Rel. 44, Last annotation update)
crystal protein crylBc (Insecticidal delta-endotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                        BEQUENCE FROM N.A.

Isakova I.A., Isakov Y.B., Rymar' S.E., Yarovoi S.V.;

Labaltied (Aug-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AVI38457; AAM93496.1; -.

R HSSP; P02965; ICIY.

R GO; GO:0005102; F:receptor binding; IEA.

GO; GO:0009405; P:pethogenesis; IEA.

R GO; GO:0009405; P:pethogenesis; IEA.

R GO; GO:0009405; P:pethogenesis; IEA.

R InterPro; IPR001178; Endotoxin.

R InterPro; IPR005639; endotoxin.

R InterPro; IPR008979; Gal bind INe.

R Ffam; PF003944; Endotoxin.C; 1.

R Ffam; PF003945; Endotoxin.C; 1.

R Pfam; PF003945; Endotoxin.N; 1.

R Pfam; PF03945; Endotoxin.N; 1.

S ERQUENCE 1231 AA; 139764 MM; C9F2848A9297EA00 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                             YMTKELEYPPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
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Name=cryIBII;
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                                                                       QSRVHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVSGPGFTGGDIIRTNV 537
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                                                                                                                                                              538 NGSVLSMGLNFNNTSLQRYRVRYRYAASQTMVLRVTVGGSTTFDQGFPSTMSANESLTSQ
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                                                                                                                                                                                                                                                                                   ||| | | : : |: : : |: SERTAGESTPENFLANAQSTFTLGAQSFSNQGVYIDRVEFVPAEVTFEAEYDLERAQKAVN
                                                                                                                                                                                                                                                                                                                                             ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        delta-endotoxin
kDa crystal protein).
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MEDLINE-96102856; PubMed-8586263;
Koo B.T., Park S.-H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIKA BACTM STANDARD; PRT; 1215 AA.

045715;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
95-UUL-2004 (Rel. 44, Last annotation update)
PSESTICATION CYPERALINE entomocidal protoxin) (137 kDa cry Name=cry1Ka; Synonyms=cry1K(a), cry1K;
Bactllus thuringiensis (subsp. morrisoni).
Bactllus firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELEYFPETDKVWIEIGETEGKFIVDSVELLLMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Burdean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@leb-sib.ch).
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                                                                                                                                                                                                                                                                                                                            the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the N- \,
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                     crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140451 MW; 7318382413529F21 CRC64;
                                                                                   Bacillus
                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: Belongs to the delta endotoxin family.
                (140 kDa
CrylB(c)) (Crystaline encompossion) (SamescrylBc; SynonymsscrylB(c), crylBc; Bacillus thuringiensis (subsp. morrisoni).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR005638; endotoxin.C.
InterPro; IPR0085639; endotoxin.N.
InterPro; IPR008979; Gal bind like.
Pfam; PP03944; Endotoxin.C; 1.
Pfam; PP03945; Endotoxin.M; 1.
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InterPro; IPR005638; endotoxin
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SEQUENCE 1233 AA;
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SEQUENCE FROM N.A.
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DT C1EB BACTA
AC 003745;
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DT 30-MAY-2000
DT 05-JUL-2004
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RN COC Bacteria; Fi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLIMVYAQAANIHILLILRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVEWYNTGL
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                                                                                                                                                                    MISCELLANEOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.1%; Score 4284.5; DB 1; Length Best Local Similarity 67.7%; Pred. No. 7.9e-261; Matches 846; Conservative 128; Mismatches 220; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1215 AA; 137378 MW; 7CAF7A3311893D9B CRC64;
                                                                                                                                                                                                           SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, 006117; 1J16.
InterPro; IPR001179; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008679; endotoxin.N.
InterPro; IPR008799; endotoxin.N.
InterPro; IPR008799; endotoxin.N.
IPEam; PF03944; Endotoxin.M.; I.
Pfam; PP03945; Endotoxin.N.; I.
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STRAIN=NRRL B-18457 / PS81A2;

STRAIN=NRRL B-19457 / PS81A2;

Repens J.M., Sick A.J.;

"Genes encoding lepidopteran-active toxins and transformed hosts.";

Patent number US5206166, 27-APR-1993.

-! FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithalial cells of many lepidopteran larvae.

-! DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
DLERAQBAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDBFCLDEKRELLEKVKYAK
                                                                                                                                                                                                 RISDERNILLODPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGSENITIQEGNDVFKE
                                                                                                                                                                                                                                                                                                       NYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDV
                                                                                                                                                                                                                                                                                                                                                                                                        807 PGTESPWPSSGVYPSGRCGEPNRCAPRIEWNPDLDCSCRYGEKCVHHSHHFSLDIDVGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  927 KRVYTEAKESVDALFVDSQYDKLQANTNIGIIHGADKQVHRIREPYLSELPVIPSINAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEELEGRIITAISLYDARNVKNGDFNNGLACWNVKGHVDVQQSHHRSVLVIPEWEAEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1047 QKVRVCPDRGYILKVTAYKEGYGEGCVTIHEFEDNTDVLKFRNFVEEEVYPNNTVTCNDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTSOSFRFA-----EFPVGISASGSQTAGISISNNAGRQTFHFDKIEFIPITATFEAEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGTESVWPLSVESPIGRCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLHENLGVWVVFKIKTOEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLOLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRVYTEAKEAVDALFVDSOYNRLOADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKPKNCBEBEVYPTDTGTCNDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1128 TAHQ----GTAVCNSRNAGYEDA----YEVDTTASVNYKPTYEBETYTDVRRDNHCEYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
50-JUL-2004 (Rel. 44, Last annotation update)
65-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylEb (Insecticidal delta-endotoxin CrylE(b)) (Crystaline entomocidal protoxin) (134 kDa crystal protein)
Name-crylEb; Synonyms-crylE(b);
Bacteria; Synonyms-crylE(b);
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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784 903 844 963

682 783 724

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DSQYNRLQADTNIGMIHAADKLVHRIREAYLSELSVIPGVNAEIFEELEGRIITAISLYD 1023
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                                                                                                                                                                                                                                    INKOPDFISTNEQSNFTSIHEQSEHGWGSENITIQEGNDVFKENYVTLPGTFNECYPTY
                                                                      RCGEPNRCAPHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDIGCTDLHENLGVWVVFKIKT
                                                                                                                                                                                 QEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFV
                                                                                                                                                                                                                                                                                         TAYKEGYGEGCVTIHEIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQGTA----VCNS
                                                                                                                                                                                                                                                                                                                                                                                                       RNAGYEDAYEVDTTASVNYKPTYEBETYTDVRRDNHCEYDRGYVNYPPLPAGYMTKELEY
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C STRANG-KI;
C STRANG-KI;
C LIM.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;
L Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
R INTER-PRO; IPRO1178; Endotoxin.
R INTER-PRO; IPRO15639; endotoxin.C.
R INTER-PRO; IPRO15639; endotoxin.C.
R INTER-PRO; IPRO15639; endotoxin.N.
R INTER-PRO; IPRO15639; endotoxin.N.
R INTER-PRO; IPRO15639; endotoxin.N.
R PEam; PF03444; Endotoxin.C;
R PEam; PF0355; Endotoxin.C;
R PEam; PF0355; Endotoxin.C;
R PEam; PF0355; Endotoxin.N; I.
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05-JUL-2004 (TrENBLrel. 27, Last sequence update)
05-JUL-2004 (TrENBLrel. 27, Last annotation update)
05-JUL-2004 (TrENBLrel. 27, Last annotation update)
05-JUL-2004 (TrENBLrel. 27, Last annotation update)
Bacillus thuringiensis (subsp. kurstaki).
Bacteria; Firmicutes; Bacillales; Bacillus.
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756; Conservative
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 WPRGRDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDAR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRSVLYTQYIALELDFINAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEFGLT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQBIQRYYERQVEQTRDYSDYCVEWYNTGLNSL-RGTNAASWVRYNQFRRDLTLGVLDLV 268
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                                                                                                                                                                                                                                                                                                                                                                                                              :: | | | :: : | :: | | | | :: ENQCIPYNCLNNPEVELLGIERSNSNVAAEIGLGLSRLLVSRIFLGDFILGLFDVIWGAI 65
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MISCELLANEOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                     Query Match 61.4%; Score 3977.5; DB 1; Length 1174; Best Local Similarity 64.6%; Pred. No. 1.7e-241; Matches 794; Conservative 115; Mismatches 222; Indela 99;
                                                                                                                                                                                                                                                                                                         1174 AA; 133601 MW; SEEA0BA7FD63480F CRC64;
                          SIMILARITY: Belongs to the delta endotoxin family
                                                                                                                                                                                           InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal bind Tike.
Fram; PP03944; Endotoxin C; 1.
Pfam; PP03945; Endotoxin M; 1.
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AAS93797;
26-APR-2004 (TrEMBLrel. 27, Created)
26-APR-2004 (TrEMBLrel. 27, Last sequence update)
26-APR-2004 (TrEMBLrel. 27, Last annotation update)
CrylB type crystal protein (Fragment).
Bacillus thuringiensis (Subgo, Kurstaki).
Bacteria, Firmicutes; Bacillales; Bacillacee; Bacillus, Bacillus cereus group; Bacillus thuringiensis.
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STRAIN=K1;

11 M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.

"crylB.";

Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AYS70734; AAS93797.1; -..

NON TER 849 849

SEQÜENCE 849 AA; 95886 MW; PCB98495787CF763 CRC64;
                                                                                                          / Match 60.2%; Score 3901.5; DB 2 Local Similarity 88.7%; Pred. No. 6.2e-237; les 756; Conservative 33; Mismatches 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
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                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2004 (Rel. 44, Last annotation update)
65-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylCb (Insecticidal delta-endotoxin
CrylC(b)) (Crystaline entomocidal protoxin) (133 kDa crystal protein).
Name=crylCb; Synonyms=crylC(b);
Bacilias thuringtensis (subsp. galleriae).
Bacteria; Firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         part of
                                                                                                                                                                                                                                                                                                                                                               40 CIAEGNNINPLVSASTVQTG---INIAGRILGVL---GVPFAGQIASFYSFLVGELWPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 RDQWEIFLEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLLRDASLFGSEFGLTSQEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.5%; Score 3791; DB 1; Length 11
llarity 62.3%; Pred. No. 9.6e-230;
Conservative 125; Mismatches 241; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1176 AA; 132867 MW; 108233494C2AC018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: Belongs to the delta endotoxin family.
                                                 PRT; 1176 AA
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InterPro; IRR00518; Endotoxin.C.
InterPro; IRR005539; endotoxin.C.
InterPro; IRR008579; endotoxin.N.
InterPro; IRR008479; endotoxin.C; IRC087944; Endotoxin.C; IRC087879; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC087875; Endotoxin.M; IRC08787
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PIR; A48970; A48970.
HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                                                                                           STRAIN=HD-29;
MEDLINE=93236401; PubMed=8476286;
                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sporulation; Toxin.
SEQUENCE 1176 AA;
                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A.
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762; Conserv
                                                                                                                                                                                                                                                           NCBI_TaxID=29338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             terminus,
                                               BACTG
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                                           C1CB B/
P56953
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Matches 76
RESULT 13
C1CB_BACTG
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575 530 634

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1115 EVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDTTASVNYKPTYEBETYTDVR 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1171 RDNHCEYDRGYVNYPPLPAGYMTKELEYFPFTDKVWIRIGETEGKFIVDSVBLLLMEE 1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DITIQGGNDVFKENYVTLPGTFDECYPTYLYQKIDESKLKAYTRYELRGYIEDSQDLEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      933 PELPFIPGINAIIFEELENRISTAFFLYEARNVINNGDFNNGLTCHNVKGHVDVQQSHHR
          GVLLWGIYLEPIHGVPTVRFNFRNPQNTFERGTANYSQP----YESPGLQLKDSETELPP
                                                        RILSAPFYSAPFLG--TSVLGSRGEEFMF--ALINNISPPSARYRNPG--TVDSLVSIPP
                                                                                                                                                                                                        516 NSGTSVVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVG
                                                                                                                                                                                                                                                                                                                                                                                                          BFI PI TATFEABYDLERAQEAVNAL PTNTNPRRLKTDVTDYHI DQVSNLVACLSDEPCLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWMGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGBSELKAYTRYQLRGYIEDSQDLEIY
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                                                                                                         ETTERPNYESYSHRLSHIGLISQSRVHVPVYSWTHRSADRINTISSDSITQIPLVKSFNL
                                                                                                                                                                                                                                                                                                          576 GSTTFDQGFPSTMSANESLTSQSFRFAEFPVGISASGSQT-AGISISNNAGRQTFHFDKI
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kDa crystal protein)
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylla (Insecticidal delta-e
Cryll(a)) (Crystaline entomocidal protoxin) (133 kDa cry
Name-crylla, Synonyms-cryll(a), cryET4;
Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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SEQUENCE FROM N.A.
STRAIN=NRRL B-21110 / EG5847;
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CLJA_BACTU
ID 20173 BD
AC 04573 BD
DT 30-MAY
DT 30-MAY
DT 05-JUL
DB PERLIC
GN Name=CC
SN Name=CC
NN NCBIT
CN NCBIT
NN NCBIT
RP RESULEN
RP SEQUEN
RC STRAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylJb (Insecticidal delta-endotoxin
CrylJ(b)) (Crystaline entomocidal protoxin) (134 kDa crystal protein).
Name=crylJb; Synonyms=crylJ(b), cryETl;
Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SELTREIYTSPV--SEYYYGAINNYNQN----GIQTERQIRQPHLMDFFNTMTMYTSYN
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                                                                                                                                                                                                                                                                                                                                                    Patent number US5356623, 18-OCT-1994.
-1- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
epithelial cells of many lepidopteran larvae. Toxic to Plutella
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                                                                                                                                                                                                                                                                                                                                                                                                                              xylostella.
DEVELOPMENTAL STAGE: The crystal protein is produced during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sporulation and is accumulated both as an inclusion and as
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=NRRL B-18973 / EG5092;
von Tersch M.A., Gonzalez J.M. Jr.;
"Bacillus thuringensis cryET1 toxin gene and protein toxic lepidopteran insects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 55.2%; Score 3579; DB 1; Length 1 al Similarity 60.5%; Pred. No. 2.2e-216; 725; Conservative 125; Mismatches 275; Indels
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InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal bind_Tike.
Pfam; PP00555; Endotoxin_C; 1.
Pfam; PP00555; Endotoxin_M; 1.
Pfam; PP03945; Endotoxin_M; 1.
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Best Local Similarity
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"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
toxic to legoldopteran insects.";
Patent number US5322697, 21-JUN-1994.
-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
epithelial cells of many lepidopteran larvae.
-I- DEVELOPMENTAL STAGE: The crystal protein is produced during
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-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
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                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the delta endotoxin family.
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InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal bind Tike.
Pfam; PP00555; Endotoxin.C; 1.
Pfam; PP00555; Endotoxin.M; 1.
Pfam; PP03945; Endotoxin.M; 1.
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SEQUENCE 1167 AA; 132760 MW;
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         FCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGW
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                                                                        WGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQLRGYIEDSQD
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